



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 164940

TO: Sarvamangala Devi
Art Unit: 1645
Location: REM-3C18
Serial Number: 10/606618

Wednesday, April 26, 2006

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Your queries have completed processing. You may access an electronic version via eDAN (SCORE) and /or <http://es/ScoreAccessWeb>.

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).



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184940

Shears, Beverly

From: Devi, Sarvamangala
Sent: Tuesday, April 11, 2006 2:42 PM
To: STIC-Biotech/ChemLib
Cc: Shears, Beverly
Subject: 10/606,618

Please ask Ms. Beverly Shears to perform this search.

In application 10/606,618, please perform a sequence search for an at least eight amino acid-long peptide of SEQ ID NO: 4 in commercial and pending application databases.

Thanx.

S. DEVI, Ph.D.
Primary Examiner
AU 1645
Rems - 3C18

2

Date completed: _____	Search Site	Vendors
Searcher: <u>Beverly e 2528</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: _____	<input type="checkbox"/> CM-1	<input type="checkbox"/> STN
Elapsed time: _____	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: _____	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
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Number of Databases: _____	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>CA</u>

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 12, 2006, 16:23:33 ; Search time 48 Seconds
(without alignments)
1372.761 Million cells

Title: US-10-606-618-4

Perfect score: 79

Sequence: 1 MKLKOIASALMMLGISPLAF.....LKKKPEDEIQRFQFQLGTTF 797

Scoring table: OLIGO

scoring metric: $\text{Gapop } 60.0$, $\text{Gapext } 60.0$

Searched: 572060 seqs. 82675679 residues

Word size : 1

total number of hits satisfying chosen parameters: 566853

Minimum DB seq length: 0

Minimum DB seq length:	0
Maximum DB seq length:	2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	ID	Description
1	797	100.0	797	2	US-09-594-192-4	Sequence 4, Appli
2	157	19.7	792	2	US-09-594-192-2	Sequence 2, Appli
3	8	1.0	94	2	US-09-489-039A-8163	Sequence 8163, Ap
4	8	1.0	97	2	US-09-205-858-1092	Sequence 1092, Ap
5	4	1.0	97	2	US-10-004-860-1092	Sequence 1092, Ap
6	8	1.0	230	2	US-09-270-767-45805	Sequence 45805, A
7	8	1.0	274	2	US-09-502-540-15552	Sequence 15552, A
8	1.0	648	2	US-09-452-591A-24628	Sequence 24628, A	
9	8	1.0	1589	2	US-09-543-681A-4998	Sequence 4998, Ap
10	7	0.9	23	2	US-09-674-973A-147	Sequence 147, App
11	7	0.9	58	2	US-08-971-089-10	Sequence 10, Appl
12	7	0.9	58	2	US-10-117-604A-10	Sequence 10, Appl
13	7	0.9	60	2	US-09-513-999C-7231	Sequence 7231, Ap
14	7	0.9	86	2	US-09-328-352-6252	Sequence 6252, Ap
15	7	0.9	86	2	US-09-489-039A-10485	Sequence 10485, A
16	7	0.9	88	2	US-09-461-325-325	Sequence 325, App
17	7	0.9	88	2	US-10-012-542-325	Sequence 325, App
18	7	0.9	88	2	US-10-115-123-325	Sequence 325, App
19	7	0.9	97	2	US-09-452-591A-18360	Sequence 18360, A
20	7	0.9	106	2	US-09-270-767-62368	Sequence 62368, A
21	7	0.9	110	2	US-09-513-999C-6601	Sequence 6601, Ap
22	7	0.9	129	2	US-09-543-681A-5037	Sequence 5037, Ap
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103	7	0.9	568	2	US-09-949-016-10896	Sequence 10896, A	176	7	0.9	1434	2	US-09-754-032-10	Sequence 10, Appl
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276	6	0.8	51	1	US-08-209-747-20	Sequence 20, Appl	349	6	0.8	87	2	US-09-270-767-48049	Sequence 48049, A
277	6	0.8	51	1	US-08-209-747-30	Sequence 30, Appl	350	6	0.8	88	2	US-09-489-039A-10714	Sequence 10714, A
278	6	0.8	51	1	US-08-458-298-20	Sequence 20, Appl	351	6	0.8	88	2	US-09-687-637B-29	Sequence 29, Appl
279	6	0.8	51	1	US-08-458-298-30	Sequence 30, Appl	352	6	0.8	89	2	US-09-687-637B-30	Sequence 30, Appl
280	6	0.8	52	1	US-09-277-078-46	Sequence 46, Appl	353	6	0.8	90	1	US-08-209-747-16	Sequence 16, Appl
281	6	0.8	52	1	US-08-209-747-25	Sequence 25, Appl	354	6	0.8	90	1	US-08-458-298-16	Sequence 16, Appl
282	6	0.8	55	1	US-08-458-298-25	Sequence 25, Appl	355	6	0.8	92	2	US-09-621-976-4742	Sequence 4742, Ap
283	6	0.8	56	2	US-08-936-165A-332	Sequence 332, App	356	6	0.8	96	2	US-09-107-532A-6122	Sequence 1, Appl
284	6	0.8	56	2	US-09-621-976-5925	Sequence 5925, Ap	357	6	0.8	98	2	US-09-147-875A-1	Sequence 9, Appl
285	6	0.8	57	2	US-09-270-767-57982	Sequence 57982, A	358	6	0.8	99	1	US-08-710-749-9	Sequence 10, Appl
286	6	0.8	57	2	US-09-006-428A-5	Sequence 5, Appl	359	6	0.8	99	1	US-08-710-749-10	Sequence 11, Appl
287	6	0.8	57	2	US-09-615-387C-5	Sequence 5, Appl	360	6	0.8	99	1	US-08-710-749-11	Sequence 11, Appl
288	6	0.8	58	2	US-09-270-767-57771	Sequence 57771, A	361	6	0.8	99	2	US-09-732-210-1583	Sequence 11, Appl
289	6	0.8	59	2	US-09-621-976-6937	Sequence 6937, Ap	362	6	0.8	99	2	US-09-147-875A-11	Sequence 14, Appl
290	6	0.8	59	2	US-09-270-767-61138	Sequence 61138, A	363	6	0.8	99	2	US-09-147-875A-14	Sequence 15, Appl
291	6	0.8	60	2	US-08-928-213B-70	Sequence 70, Appl	364	6	0.8	99	2	US-09-147-875A-15	Sequence 16, Appl
292	6	0.8	60	2	US-09-248-796A-25960	Sequence 25960, A	365	6	0.8	99	2	US-09-147-875A-16	Sequence 19, Appl
293	6	0.8	61	2	US-09-248-796A-24801	Sequence 24801, A	366	6	0.8	100	1	US-08-308-494A-19	Sequence 4, Appl
294	6	0.8	61	2	US-09-248-796A-26402	Sequence 26402, A	367	6	0.8	100	2	US-09-147-875A-8	Sequence 8, Appl
295	6	0.8	63	2	US-09-673-395A-403	Sequence 403, App	368	6	0.8	100	2	US-09-147-875A-10	Sequence 12, Appl
296	6	0.8	64	1	US-08-209-521-20	Sequence 20, Appl	369	6	0.8	100	2	US-09-147-875A-12	Sequence 3, Appl
297	6	0.8	64	2	US-08-961-810-130	Sequence 130, App	370	6	0.8	101	1	US-08-710-749-3	Sequence 7, Appl
298	6	0.8	64	2	US-08-352-902D-130	Sequence 130, App	371	6	0.8	101	1	US-08-710-749-7	Sequence 9, Appl
299	6	0.8	64	2	US-09-265-503B-130	Sequence 130, App	372	6	0.8	101	2	US-09-147-875A-9	Sequence 1, Appl
300	6	0.8	64	2	US-09-270-767-61944	Sequence 61944, A	373	6	0.8	101	2	US-08-169-701-1	Sequence 8, Appl
301	6	0.8	65	2	US-09-248-796A-25471	Sequence 25471, A	374	6	0.8	102	1	US-08-710-749-8	Sequence 21, Appl
302	6	0.8	65	2	US-09-640-211A-604	Sequence 604, App	375	6	0.8	102	1	US-08-710-749-21	Sequence 1, Appl
303	6	0.8	65	2	US-09-621-976-4488	Sequence 4488, Ap	376	6	0.8	102	1	US-08-760-903-1	Sequence 1, Appl
304	6	0.8	66	2	US-09-270-767-60792	Sequence 60792, A	377	6	0.8	102	1	US-08-482-191-1	Sequence 18, Appl
305	6	0.8	67	2	US-09-248-796A-23279	Sequence 23279, A	378	6	0.8	102	2	US-09-147-875A-18	Sequence 57873, A
306	6	0.8	68	2	US-09-252-991A-30574	Sequence 30574, A	379	6	0.8	102	2	US-09-270-767-57873	Sequence 14676, A
307	6	0.8	68	2	US-09-489-039A-11466	Sequence 11466, A	380	6	0.8	102	2	US-09-902-540-14676	Sequence 1, Appl
308	6	0.8	68	2	US-09-902-540-11724	Sequence 11724, A	381	6	0.8	102	4	PCT-US96-10227-1	Sequence 4, Appl
309	6	0.8	69	2	US-09-732-210-11004	Sequence 1004, Ap	382	6	0.8	103	1	US-08-467-393-4	Sequence 4, Appl
310	6	0.8	70	1	US-08-691-814B-34	Sequence 34, Appl	383	6	0.8	103	1	US-08-209-747-4	Sequence 19, Appl
311	6	0.8	70	2	US-09-732-210-883	Sequence 883, App	384	6	0.8	103	1	US-08-458-298-4	Sequence 20, Appl
312	6	0.8	70	2	US-09-621-976-5508	Sequence 5508, Ap	385	6	0.8	104	1	US-08-710-749-19	Sequence 5, Appl
313	6	0.8	70	6	5453566-2	Patent No. 5453566	386	6	0.8	104	2	US-08-479-089A-5	Sequence 6, Appl
314	6	0.8	71	2	US-09-732-210-93	Sequence 93, Appl	387	6	0.8	104	2	US-08-710-749-20	Sequence 20, Appl
315	6	0.8	71	2	US-09-270-767-56690	Sequence 56690, A	388	6	0.8	104	2	US-08-479-089A-6	Sequence 5, Appl
316	6	0.8	73	2	US-09-949-016-8499	Sequence 8499, Ap	389	6	0.8	104	2	US-07-669-545B-5	Sequence 6, Appl
317	6	0.8	73	2	US-09-489-039A-12244	Sequence 12244, A	390	6	0.8	104	2	US-07-669-545B-6	Sequence 20, Appl
318	6	0.8	73	2	US-09-902-540-10252	Sequence 10252, A	391	6	0.8	104	2	US-09-147-875A-20	
319	6	0.8	74	2	US-09-543-681A-8341	Sequence 8341, Ap	392	6	0.8	104	2		

393	6	0.8	104	2	US-09-147-875A-21	Sequence 21, Appl	466	6	0.8	110	2	US-09-107-532A-6721	Sequence 6721, Ap
394	6	0.8	105	1	US-08-889-013C-6	Sequence 6, Appl	467	6	0.8	110	2	US-09-489-038A-10081	Sequence 10081, A
395	6	0.8	105	2	US-09-205-258-1082	Sequence 1082, Ap	468	6	0.8	110	2	US-09-902-540-11433	Sequence 11433, A
396	6	0.8	105	2	US-09-583-110-5144	Sequence 5144, Ap	469	6	0.8	112	2	US-09-543-681A-4827	Sequence 4827, Ap
397	6	0.8	105	2	US-09-640-211A-924	Sequence 924, App	470	6	0.8	112	2	US-09-710-279-2114	Sequence 2114, Ap
398	6	0.8	105	2	US-09-640-211A-2239	Sequence 2239, Ap	471	6	0.8	113	1	US-08-256-568B-85	Sequence 85, Appl
399	6	0.8	105	2	US-10-004-860-1082	Sequence 1082, Ap	472	6	0.8	113	2	US-09-038-369B-85	Sequence 85, Appl
400	6	0.8	106	1	US-07-732-242C-2	Sequence 2, Appl	473	6	0.8	113	2	US-08-836-075A-82	Sequence 82, Appl
401	6	0.8	106	1	US-08-290-592B-34	Sequence 34, Appl	474	6	0.8	113	2	US-08-836-075A-98	Sequence 98, Appl
402	6	0.8	106	1	US-08-290-592B-35	Sequence 35, Appl	475	6	0.8	113	2	US-09-378-900A-85	Sequence 85, Appl
403	6	0.8	106	1	US-08-956-047-33	Sequence 33, Appl	476	6	0.8	113	2	US-09-899-044-85	Sequence 85, Appl
404	6	0.8	106	2	US-08-397-411-8	Sequence 8, Appl	477	6	0.8	113	2	US-09-489-039A-8131	Sequence 8131, Ap
405	6	0.8	106	2	US-08-397-411-9	Sequence 9, Appl	478	6	0.8	113	2	US-09-878-281A-218	Sequence 218, App
406	6	0.8	106	2	US-09-771-415-1	Sequence 1, Appl	479	6	0.8	113	2	US-09-899-302-85	Sequence 85, Appl
407	6	0.8	106	2	US-09-771-415-17	Sequence 17, Appl	480	6	0.8	113	2	US-09-899-082B-85	Sequence 85, Appl
408	6	0.8	106	2	US-09-232-290-24	Sequence 24, Appl	481	6	0.8	113	2	US-09-899-082B-124	Sequence 124, App
409	6	0.8	106	2	US-09-996-288-8	Sequence 8, Appl	482	6	0.8	113	2	US-09-899-082B-125	Sequence 125, App
410	6	0.8	106	2	US-09-996-288-11	Sequence 11, Appl	483	6	0.8	114	2	US-09-710-279-2252	Sequence 2252, Ap
411	6	0.8	106	2	US-09-996-288-54	Sequence 54, Appl	484	6	0.8	114	2	US-09-513-999C-5777	Sequence 5777, Ap
412	6	0.8	106	2	US-09-996-265-8	Sequence 8, Appl	485	6	0.8	117	1	US-08-274-661B-38	Sequence 38, Appl
413	6	0.8	106	2	US-09-996-265-11	Sequence 11, Appl	486	6	0.8	117	2	US-09-513-999C-6175	Sequence 6175, Ap
414	6	0.8	106	2	PCT-US95-265-54	Sequence 54, Appl	487	6	0.8	119	2	US-09-732-210-678	Sequence 678, App
415	6	0.8	106	4	PCT-US95-10053-31	Sequence 31, Appl	488	6	0.8	119	2	US-09-270-767-47348	Sequence 47348, A
416	6	0.8	106	4	PCT-US95-10053-32	Sequence 32, Appl	489	6	0.8	119	2	US-09-830-954A-28	Sequence 28, Appl
417	6	0.8	106	4	PCT-US96-09448-34	Sequence 34, Appl	490	6	0.8	120	2	US-09-308-345A-21	Sequence 21, Appl
418	6	0.8	106	4	PCT-US96-09448-35	Sequence 35, Appl	491	6	0.8	122	2	US-09-198-452A-510	Sequence 510, App
419	6	0.8	107	1	US-07-942-245-3	Sequence 3, Appl	492	6	0.8	122	2	US-09-270-767-33422	Sequence 33422, A
420	6	0.8	107	1	US-08-303-569B-25	Sequence 25, Appl	493	6	0.8	122	2	US-09-270-767-48639	Sequence 48639, A
421	6	0.8	107	1	US-08-303-569B-26	Sequence 26, Appl	494	6	0.8	122	2	US-09-902-540-13323	Sequence 13323, A
422	6	0.8	107	1	US-08-303-569B-27	Sequence 27, Appl	495	6	0.8	123	2	US-09-198-452A-625	Sequence 625, App
423	6	0.8	107	1	US-08-303-569B-28	Sequence 28, Appl	496	6	0.8	123	2	US-09-270-767-43402	Sequence 43402, A
424	6	0.8	107	1	US-08-303-569B-29	Sequence 29, Appl	497	6	0.8	123	2	US-09-438-185A-585	Sequence 585, App
425	6	0.8	107	1	US-08-070-116A-6	Sequence 6, Appl	498	6	0.8	124	2	US-09-509-738C-15	Sequence 15, Appl
426	6	0.8	107	1	US-08-070-116A-8	Sequence 8, Appl	499	6	0.8	126	1	US-08-656-586-6	Sequence 6, Appl
427	6	0.8	107	1	US-08-070-116A-9	Sequence 9, Appl	500	6	0.8	126	2	US-09-663-600A-102	Sequence 102, App
428	6	0.8	107	1	US-08-070-116A-18	Sequence 18, Appl	501	6	0.8	126	2	US-09-270-767-41467	Sequence 41467, A
429	6	0.8	107	1	US-08-116-247-8	Sequence 8, Appl	502	6	0.8	126	2	US-09-270-767-58058	Sequence 58058, A
430	6	0.8	107	1	US-08-116-247-26	Sequence 26, Appl	503	6	0.8	128	1	US-08-656-586-2	Sequence 2, Appl
431	6	0.8	107	1	US-08-116-247-27	Sequence 27, Appl	504	6	0.8	128	1	US-08-956-047-31	Sequence 31, Appl
432	6	0.8	107	1	US-08-116-247-28	Sequence 28, Appl	505	6	0.8	128	2	US-08-444-644-25	Sequence 25, Appl
433	6	0.8	107	1	US-08-116-247-29	Sequence 29, Appl	506	6	0.8	128	2	US-08-232-246A-25	Sequence 25, Appl
434	6	0.8	107	2	US-09-370-838-113	Sequence 113, App	507	6	0.8	128	2	US-09-134-001C-4164	Sequence 4164, Ap
435	6	0.8	107	2	US-08-557-050-6	Sequence 6, Appl	508	6	0.8	128	2	US-09-270-767-57599	Sequence 57599, A
436	6	0.8	107	2	US-08-557-050-8	Sequence 8, Appl	509	6	0.8	129	2	US-09-134-000C-5429	Sequence 5429, Ap
437	6	0.8	107	2	US-08-557-050-9	Sequence 9, Appl	510	6	0.8	129	2	US-09-513-999C-5540	Sequence 5540, Ap
438	6	0.8	107	2	US-09-795-515-25	Sequence 25, Appl	511	6	0.8	129	2	US-09-513-999C-8080	Sequence 8080, Ap
439	6	0.8	107	2	US-09-795-515-26	Sequence 26, Appl	512	6	0.8	129	2	US-09-902-540-12956	Sequence 12956, A
440	6	0.8	107	2	US-09-795-515-27	Sequence 27, Appl	513	6	0.8	131	2	US-09-270-767-38194	Sequence 38194, A
441	6	0.8	107	2	US-09-795-515-28	Sequence 28, Appl	514	6	0.8	131	2	US-09-270-767-53411	Sequence 53411, A
442	6	0.8	107	2	US-09-795-515-29	Sequence 29, Appl	515	6	0.8	133	2	US-09-621-976-6550	Sequence 6550, Ap
443	6	0.8	107	2	US-09-348-224-8	Sequence 8, Appl	516	6	0.8	134	2	US-08-529-055-65	Sequence 65, Appl
444	6	0.8	107	2	US-09-348-224-26	Sequence 26, Appl	517	6	0.8	134	2	US-09-248-796A-27186	Sequence 27186, A
445	6	0.8	107	2	US-09-348-224-27	Sequence 27, Appl	518	6	0.8	134	2	US-10-104-047-2098	Sequence 2098, Ap
446	6	0.8	107	2	US-09-348-224-28	Sequence 28, Appl	519	6	0.8	135	2	US-09-252-991A-22092	Sequence 22092, A
447	6	0.8	107	2	US-09-348-224-29	Sequence 29, Appl	520	6	0.8	135	2	US-09-252-991A-22092	Sequence 5156, Ap
448	6	0.8	107	2	US-09-854-133-113	Sequence 113, App	521	6	0.8	136	2	US-09-107-433-5156	Sequence 39814, A
449	6	0.8	107	4	PCT-US91-01360-3	Sequence 3, Appl	522	6	0.8	136	2	US-09-270-767-59314	Sequence 59314, A
450	6	0.8	108	1	US-08-710-749-24	Sequence 24, Appl	523	6	0.8	137	2	US-09-270-767-59338	Sequence 59338, A
451	6	0.8	108	2	US-09-147-875A-25	Sequence 25, Appl	524	6	0.8	137	2	US-09-472-087-79	Sequence 79, Appl
452	6	0.8	108	2	US-09-726-219A-241	Sequence 241, App	525	6	0.8	138	2	US-09-270-767-57429	Sequence 57429, A
453	6	0.8	108	2	US-09-726-219A-242	Sequence 242, App	526	6	0.8	138	2	US-09-252-991A-25939	Sequence 25939, A
454	6	0.8	108	2	US-09-726-219A-243	Sequence 243, App	527	6	0.8	139	2	US-09-902-540-10025	Sequence 10025, A
455	6	0.8	108	2	US-09-726-219A-251	Sequence 251, App	528	6	0.8	139	2	US-09-998-805-3	Sequence 3, Appl
456	6	0.8	108	2	US-09-726-219A-252	Sequence 252, App	529	6	0.8	140	2	US-09-248-796A-27587	Sequence 27587, A
457	6	0.8	108	2	US-09-726-219A-253	Sequence 253, App	530	6	0.8	141	2	US-09-286-981B-2	Sequence 2, Appl
458	6	0.8	108	2	US-09-196-522-241	Sequence 241, App	531	6	0.8	141	2	US-09-270-767-43497	Sequence 43497, A
459	6	0.8	108	2	US-09-196-522-242	Sequence 242, App	532	6	0.8	141	2	US-10-254-995-2	Sequence 2, Appl
460	6	0.8	108	2	US-09-196-522-243	Sequence 243, App	533	6	0.8	142	2	US-09-252-991A-27627	Sequence 27627, A
461	6	0.8	108	2	US-09-196-522-251	Sequence 251, App	534	6	0.8	142	2	US-09-039-859-7	Sequence 7, Appl
462	6	0.8	108	2	US-09-196-522-252	Sequence 252, App	535	6	0.8	143	2	US-09-252-991A-22066	Sequence 22066, A
463	6	0.8	108	2	US-09-196-522-253	Sequence 253, App	536	6	0.8	143	2	US-09-252-991A-29827	Sequence 29827, A
464	6	0.8	110	2	US-08-836-561-33	Sequence 33, Appl	537	6	0.8	143	2	US-09-133-979A-21	Sequence 21, Appl
465	6	0.8	110	2	US-09-434-122-33	Sequence 33, Appl	538	6	0.8	144	1		

539	6	0.8	144	1	US-08-436-930-21	Sequence 21, Appl	612	169	2	US-09-248-796A-26743	Sequence 26743, A
540	6	0.8	144	1	US-08-451-213-21	Sequence 21, Appl	613	170	2	US-09-732-210-558	Sequence 558, App
541	6	0.8	144	2	US-10-104-047-3457	Sequence 3457, App	614	170	2	US-08-529-055-60	Sequence 60, Appl
542	6	0.8	145	2	US-09-602-787A-330	Sequence 330, App	615	171	2	US-09-248-796A-27723	Sequence 27723, A
543	6	0.8	145	2	US-09-640-211A-698	Sequence 698, App	616	172	2	US-09-583-110-3305	Sequence 3305, Ap
544	6	0.8	145	2	US-09-902-540-13747	Sequence 13747, A	617	173	2	US-09-270-767-32051	Sequence 32051, A
545	6	0.8	146	2	US-09-252-91A-24703	Sequence 24703, A	618	173	2	US-09-270-767-47268	Sequence 47268, A
546	6	0.8	146	2	US-09-902-540-13495	Sequence 13495, A	619	174	2	US-09-149-476-413	Sequence 413, App
547	6	0.8	147	2	US-09-602-787A-332	Sequence 332, App	620	174	2	US-09-270-767-40521	Sequence 40521, A
548	6	0.8	148	2	US-08-857-076-17	Sequence 8000, Ap	621	174	2	US-09-270-767-55737	Sequence 55737, A
549	6	0.8	150	2	US-08-857-076-17	Sequence 17, Appl	622	175	2	US-09-252-991A-28806	Sequence 28806, A
550	6	0.8	150	2	US-09-663-600A-196	Sequence 196, App	623	175	2	US-09-270-767-32224	Sequence 32224, A
551	6	0.8	150	2	US-09-663-600A-196	Sequence 12171, A	624	176	2	US-09-780-717-2	Sequence 2, Appl
552	6	0.8	150	2	US-09-205-658-17	Sequence 17, Appl	625	176	2	US-09-248-796A-20163	Sequence 20163, A
553	6	0.8	151	2	US-09-252-991A-16814	Sequence 16814, Ap	626	177	2	US-09-248-796A-25947	Sequence 25947, A
554	6	0.8	151	2	US-09-328-352-5751	Sequence 5751, Ap	627	178	2	US-09-248-796A-24917	Sequence 24917, A
555	6	0.8	151	2	US-09-540-236-2801	Sequence 2801, Ap	628	178	2	US-08-671-548C-14	Sequence 14, Appl
556	6	0.8	151	2	US-09-248-796A-16825	Sequence 16825, A	629	180	2	US-09-732-210-1077	Sequence 1077, Ap
557	6	0.8	152	2	US-09-270-767-48811	Sequence 48811, A	630	180	2	US-08-284-667A-14	Sequence 14, Appl
558	6	0.8	153	2	US-09-732-210-1748	Sequence 1748, Ap	631	181	2	US-09-252-991A-17913	Sequence 17913, A
559	6	0.8	153	2	US-09-270-767-32681	Sequence 32681, A	632	182	1	US-08-529-055-42	Sequence 42, Appl
560	6	0.8	153	2	US-09-270-767-47898	Sequence 47898, A	633	182	2	US-08-529-055-42	Sequence 93, Appl
561	6	0.8	153	2	US-09-902-540-12086	Sequence 12086, A	634	182	2	US-08-529-055-50	Sequence 50, Appl
562	6	0.8	155	1	US-08-209-747-15	Sequence 15, Appl	635	183	2	US-09-122-443-13	Sequence 13, Appl
563	6	0.8	155	2	US-08-458-298-15	Sequence 15, Appl	636	184	2	US-09-558-089-13	Sequence 13, Appl
564	6	0.8	155	2	US-09-489-039A-7828	Sequence 7828, Ap	637	184	2	US-09-558-089-13	Sequence 13, Appl
565	6	0.8	156	2	US-09-134-000C-6299	Sequence 6299, Ap	638	184	2	US-09-558-089-13	Sequence 13, Appl
566	6	0.8	157	2	US-09-328-352-4165	Sequence 4165, Ap	639	184	2	US-09-558-089-13	Sequence 13, Appl
567	6	0.8	157	2	US-09-902-540-14881	Sequence 14881, A	640	185	2	US-09-558-089-13	Sequence 13, Appl
568	6	0.8	158	2	US-09-252-991A-29352	Sequence 29352, A	641	186	2	US-08-529-055-46	Sequence 46, Appl
569	6	0.8	158	2	US-09-134-000C-4025	Sequence 4025, Ap	642	187	2	US-09-248-796A-19329	Sequence 19329, A
570	6	0.8	158	2	US-09-265-585C-130	Sequence 130, App	643	188	2	US-09-489-039A-13533	Sequence 13533, A
571	6	0.8	159	2	US-09-252-991A-22914	Sequence 22914, A	644	188	2	US-09-902-540-12348	Sequence 12348, A
572	6	0.8	159	2	US-09-602-787A-102	Sequence 102, App	645	188	2	US-09-252-991A-30049	Sequence 30049, A
573	6	0.8	159	2	US-09-270-767-37981	Sequence 37981, A	646	189	2	US-08-671-548C-2	Sequence 2, Appl
574	6	0.8	159	2	US-09-270-767-46525	Sequence 46525, A	647	191	2	US-09-252-991A-24515	Sequence 24515, A
575	6	0.8	159	2	US-09-270-767-53198	Sequence 53198, A	648	191	2	US-09-328-352-6761	Sequence 6761, Ap
576	6	0.8	160	2	US-09-117-257-38	Sequence 38, Appl	649	191	2	US-09-640-211A-1080	Sequence 1080, Ap
577	6	0.8	160	2	US-09-489-352-38	Sequence 38, Appl	650	191	2	US-08-284-667A-2	Sequence 2, Appl
578	6	0.8	160	2	US-08-858-207A-322	Sequence 322, App	651	192	2	US-09-149-476-419	Sequence 419, App
579	6	0.8	160	2	US-09-252-991A-16641	Sequence 16641, A	652	192	2	US-09-543-681A-7846	Sequence 7846, Ap
580	6	0.8	160	2	US-09-621-976-6030	Sequence 6030, Ap	653	192	2	US-08-671-548C-16	Sequence 16, Appl
581	6	0.8	160	2	US-09-270-767-39354	Sequence 39354, A	654	193	2	US-08-284-667A-16	Sequence 16, Appl
582	6	0.8	160	2	US-09-270-767-45565	Sequence 45565, A	655	193	2	US-08-284-667A-16	Sequence 16, Appl
583	6	0.8	160	2	US-09-270-767-54571	Sequence 54571, A	656	194	2	US-09-248-796A-27860	Sequence 27860, A
584	6	0.8	161	2	US-09-902-540-10892	Sequence 10892, A	657	195	1	US-08-403-852D-24	Sequence 24, Appl
585	6	0.8	161	2	US-09-902-540-16115	Sequence 16115, A	658	195	2	US-08-510-646B-25	Sequence 25, Appl
586	6	0.8	162	2	US-09-446-504-27	Sequence 27, Appl	659	195	2	US-09-231-818-24	Sequence 24, Appl
587	6	0.8	162	2	US-09-712-266-27	Sequence 27, Appl	660	195	2	US-09-583-110-4558	Sequence 4558, Ap
588	6	0.8	162	2	US-09-499-148-5	Sequence 5, Appl	661	196	2	US-08-711-164-379	Sequence 379, App
589	6	0.8	162	2	US-09-270-767-43246	Sequence 43246, A	662	196	2	US-09-543-681A-7659	Sequence 7659, Ap
590	6	0.8	164	2	US-09-270-767-33348	Sequence 33348, A	663	197	1	US-08-779-870-1	Sequence 1, Appl
591	6	0.8	164	2	US-09-270-767-48565	Sequence 48565, A	664	197	1	US-08-529-055-44	Sequence 44, Appl
592	6	0.8	165	2	US-09-513-999C-7900	Sequence 7900, Ap	665	198	2	US-08-529-055-36	Sequence 36, Appl
593	6	0.8	166	2	US-09-252-991A-19472	Sequence 19472, A	666	198	2	US-08-529-055-61	Sequence 61, Appl
594	6	0.8	166	2	US-09-889-463A-12	Sequence 12, Appl	667	198	2	US-09-270-767-36571	Sequence 36571, A
595	6	0.8	167	2	US-09-062-440-8	Sequence 8, Appl	668	198	2	US-09-270-767-44202	Sequence 44202, A
596	6	0.8	167	2	US-09-062-440-9	Sequence 9, Appl	669	198	2	US-09-270-767-51788	Sequence 51788, A
597	6	0.8	167	2	US-09-062-440-11	Sequence 11, Appl	670	198	2	Sequence 1045, Ap	
598	6	0.8	167	2	US-09-712-495-8	Sequence 8, Appl	671	198	2	Sequence 11711, A	
599	6	0.8	167	2	US-09-712-495-9	Sequence 9, Appl	672	198	2	Sequence 32508, A	
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605	6	0.8	168	2	US-09-134-000C-4552	Sequence 4552, Ap	678	202	2	Sequence 47255, A	
606	6	0.8	168	2	US-09-398-405-30	Sequence 30, Appl	679	202	2	Sequence 47255, A	
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609	6	0.8	169	2	US-09-270-767-39082	Sequence 39082, A	682	203	2	Sequence 47255, A	
610	6	0.8	169	2	US-09-270-767-51576	Sequence 51576, A	683	204	2	Sequence 47255, A	
611	6	0.8	169	2	US-09-270-767-54299	Sequence 54299, A	684	204	2	Sequence 47255, A	

685	6	0.8	204	2	US-08-529-055-51	Sequence 51, Appl	758	234	2	US-08-836-236-4	Sequence 4, Appl
686	6	0.8	204	2	US-08-529-055-58	Sequence 58, Appl	759	234	2	US-08-836-236-5	Sequence 5, Appl
687	6	0.8	204	2	US-09-710-279-2394	Sequence 2394, Ap	760	234	2	US-08-715-628B-3	Sequence 3, Appl
688	6	0.8	205	2	US-09-710-279-3020	Sequence 3020, Ap	761	234	2	US-09-535-679-4	Sequence 4, Appl
689	6	0.8	206	2	US-09-134-001C-4621	Sequence 4621, Ap	762	234	2	US-09-535-679-5	Sequence 5, Appl
690	6	0.8	206	2	US-08-529-055-54	Sequence 54, Appl	763	235	1	US-08-190-199A-61	Sequence 61, Appl
691	6	0.8	207	2	US-09-046-894-33	Sequence 33, Appl	764	235	1	US-08-303-569B-5	Sequence 5, Appl
692	6	0.8	208	2	US-09-134-001C-4132	Sequence 4132, Ap	765	235	1	US-08-116-247-5	Sequence 5, Appl
693	6	0.8	209	2	US-09-583-110-2988	Sequence 2988, Ap	766	235	2	US-09-795-515-5	Sequence 5, Appl
694	6	0.8	209	2	US-09-107-433-3989	Sequence 3989, Ap	767	235	2	US-09-270-767-48485	Sequence 48485, A
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696	6	0.8	210	2	US-09-543-681A-7093	Sequence 7093, Ap	769	235	2	US-09-348-224-5	Sequence 5, Appl
697	6	0.8	211	2	US-09-902-540-10681	Sequence 10681, A	770	235	2	US-09-949-016-7903	Sequence 7903, Ap
698	6	0.8	212	2	US-09-543-681A-6089	Sequence 6089, Ap	771	236	1	US-08-190-199A-65	Sequence 65, Appl
699	6	0.8	212	2	US-09-248-796A-15317	Sequence 15317, A	772	236	2	US-08-411-768B-8	Sequence 8, Appl
700	6	0.8	213	1	US-08-941-263-3	Sequence 3, Appl	773	236	2	US-09-543-681A-6359	Sequence 6359, Ap
701	6	0.8	213	2	US-09-227-178-3	Sequence 3, Appl	774	236	2	US-09-827-688-2	Sequence 2, Appl
702	6	0.8	213	2	US-08-397-411-12	Sequence 12, Appl	775	237	2	US-09-320-878-11	Sequence 11, Appl
703	6	0.8	213	2	US-09-470-449-3	Sequence 3, Appl	776	237	2	US-09-105-537-18	Sequence 18, Appl
704	6	0.8	213	2	US-09-726-775-3	Sequence 3, Appl	777	237	2	US-09-216-295-19	Sequence 19, Appl
705	6	0.8	213	2	US-09-252-991A-25866	Sequence 25866, A	778	237	2	US-09-657-440-11	Sequence 11, Appl
706	6	0.8	213	2	US-08-529-055-47	Sequence 47, Appl	779	237	2	US-09-252-991A-19656	Sequence 19656, A
707	6	0.8	213	2	US-09-996-288-209	Sequence 209, App	780	237	2	US-09-543-681A-5471	Sequence 5471, Ap
708	6	0.8	213	2	US-09-996-288-231	Sequence 231, App	781	237	2	US-09-632-570-19	Sequence 19, Appl
709	6	0.8	213	2	US-09-996-288-255	Sequence 255, App	782	237	2	US-09-632-575-49	Sequence 49, Appl
710	6	0.8	213	2	US-09-603-208A-124	Sequence 124, App	783	237	2	US-09-793-708-11	Sequence 11, Appl
711	6	0.8	213	2	US-09-902-540-13705	Sequence 13705, A	784	238	2	US-09-328-352-6703	Sequence 6703, Ap
712	6	0.8	213	2	US-09-996-265-209	Sequence 209, App	785	238	2	US-09-543-681A-4429	Sequence 4429, Ap
713	6	0.8	213	2	US-09-996-265-231	Sequence 231, App	786	239	2	US-09-540-236-3366	Sequence 3366, Ap
714	6	0.8	213	2	US-09-996-265-255	Sequence 255, App	787	239	2	US-09-248-796A-15852	Sequence 15852, A
715	6	0.8	213	2	US-10-135-636-7	Sequence 7, Appl	788	239	2	US-09-107-433-3281	Sequence 3281, Ap
716	6	0.8	214	2	US-09-543-681A-6408	Sequence 6408, Ap	789	239	2	US-09-830-954A-6	Sequence 6, Appl
717	6	0.8	214	2	US-09-270-767-42972	Sequence 42972, A	790	240	1	US-08-956-047-25	Sequence 25, Appl
718	6	0.8	214	2	US-09-893-737-306	Sequence 306, App	791	240	2	US-09-540-236-2994	Sequence 2994, Ap
719	6	0.8	215	2	US-09-252-991A-22038	Sequence 22038, A	792	240	2	US-09-270-767-48132	Sequence 48132, A
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722	6	0.8	217	2	US-09-484-577A-30	Sequence 30, Appl	795	241	2	US-09-270-767-38616	Sequence 38616, A
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725	6	0.8	218	2	US-09-270-767-43455	Sequence 43455, A	798	241	2	US-09-270-767-55794	Sequence 55794, A
726	6	0.8	218	2	US-09-248-796A-16056	Sequence 16056, A	799	241	2	US-09-854-133-194	Sequence 194, App
727	6	0.8	218	2	US-09-107-433-3578	Sequence 3578, Ap	800	241	2	US-09-581-345-5	Sequence 5, Appl
728	6	0.8	218	2	US-09-902-540-13913	Sequence 13913, A	801	241	2	US-09-902-540-9790	Sequence 9790, Ap
729	6	0.8	219	1	US-08-401-068-6	Sequence 6, Appl	802	241	2	US-09-774-490-4	Sequence 4, Appl
730	6	0.8	219	1	US-08-846-338-6	Sequence 6, Appl	803	242	2	US-09-583-110-3522	Sequence 3522, Ap
731	6	0.8	219	2	US-09-198-452A-634	Sequence 634, App	804	242	2	US-09-859-392-34	Sequence 34, Appl
732	6	0.8	219	2	US-09-438-185A-593	Sequence 593, App	805	242	2	US-09-949-016-10911	Sequence 10911, A
733	6	0.8	220	2	US-09-853-450-38	Sequence 38, Appl	806	245	2	US-09-071-035-310	Sequence 310, App
734	6	0.8	221	2	US-09-198-452A-292	Sequence 292, App	807	245	2	US-10-206-576-310	Sequence 310, App
735	6	0.8	222	1	US-09-190-199A-67	Sequence 67, Appl	808	246	2	US-09-336-536-31	Sequence 31, Appl
736	6	0.8	222	2	US-09-252-991A-21377	Sequence 21377, A	809	246	2	US-09-134-000C-5137	Sequence 5137, Ap
737	6	0.8	223	1	US-08-190-199A-63	Sequence 63, Appl	810	246	2	US-09-244-805-32	Sequence 32, Appl
738	6	0.8	223	2	US-09-252-991A-17072	Sequence 17072, A	811	248	2	US-09-248-796A-18654	Sequence 18654, A
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741	6	0.8	224	2	US-09-438-185A-281	Sequence 281, App	814	248	2	US-09-902-540-11644	Sequence 11644, A
742	6	0.8	225	2	US-09-270-767-32728	Sequence 32728, A	815	248	2	US-10-012-231A-194	Sequence 194, App
743	6	0.8	225	2	US-09-270-767-47945	Sequence 47945, A	816	248	2	US-10-015-389A-194	Sequence 194, App
744	6	0.8	225	2	US-09-710-279-1594	Sequence 1594, Ap	817	248	2	US-10-006-768A-194	Sequence 194, App
745	6	0.8	226	2	US-09-252-991A-17294	Sequence 17294, A	818	248	2	US-10-015-671A-194	Sequence 194, App
746	6	0.8	226	2	US-09-270-767-60023	Sequence 60023, A	819	248	2	US-10-015-393A-194	Sequence 194, App
747	6	0.8	227	2	US-09-252-991A-30027	Sequence 30027, A	820	248	2	US-10-011-833A-194	Sequence 194, App
748	6	0.8	229	2	US-09-107-532A-6064	Sequence 6064, Ap	821	248	2	US-10-006-041A-194	Sequence 194, App
749	6	0.8	231	2	US-10-112-802-1	Sequence 1, Appl	822	248	2	US-10-012-064A-194	Sequence 194, App
750	6	0.8	231	2	US-09-270-767-43196	Sequence 43196, A	823	249	1	US-08-685-992-8	Sequence 8, Appl
751	6	0.8	232	2	US-08-529-055-70	Sequence 70, Appl	824	249	1	US-09-144-925-8	Sequence 8, Appl
752	6	0.8	232	2	US-09-248-796A-14122	Sequence 14122, A	825	249	2	US-09-949-016-8151	Sequence 8151, Ap
753	6	0.8	233	2	US-09-252-991A-20802	Sequence 20802, A	826	250	2	US-09-489-039A-9843	Sequence 9843, Ap
754	6	0.8	233	2	US-09-252-991A-21274	Sequence 21274, A	827	250	2	US-09-134-000C-4602	Sequence 4602, Ap
755	6	0.8	233	2	US-09-252-991A-23516	Sequence 23516, A	828	251	1	US-08-209-747-8	Sequence 8, Appl
756	6	0.8	233	2	US-09-270-767-43719	Sequence 43719, A	829	251	1	US-08-458-298-8	Sequence 8, Appl
757	6	0.8	233	2	US-09-605-703B-2398	Sequence 2388, Ap	830	251	2	US-09-902-540-15293	Sequence 15293, A

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832	6	0.8	252	2	US-09-583-110-3303	Sequence 3303, Ap	905	276	2	US-09-765-272A-134	Sequence 134, App
833	6	0.8	252	2	US-09-270-767-47090	Sequence 47090, A	906	279	2	US-09-314-701-60	Sequence 60, Appl
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835	6	0.8	253	2	US-09-902-540-14305	Sequence 14305, A	908	279	2	US-09-270-767-33415	Sequence 33415, A
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838	6	0.8	254	2	US-09-586-106D-159	Sequence 159, App	911	279	2	US-10-314-639-60	Sequence 60, Appl
839	6	0.8	254	2	US-09-949-016-6948	Sequence 6948, Ap	912	279	2	US-10-059-964A-60	Sequence 7715, Ap
840	6	0.8	254	2	US-10-799-870-159	Sequence 870, App	913	280	2	US-09-489-039A-7715	Sequence 4231, Ap
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846	6	0.8	256	2	US-09-089-019-12	Sequence 12, Appl	919	284	1	US-08-592-214A-24	Sequence 20, Appl
847	6	0.8	256	2	US-09-252-991A-32307	Sequence 32307, A	920	284	2	US-08-659-188-20	Sequence 20, Appl
848	6	0.8	256	2	US-09-107-532A-3657	Sequence 3657, Ap	921	284	2	US-08-655-227-20	Sequence 20, Appl
849	6	0.8	256	2	US-09-583-110-4113	Sequence 4113, Ap	922	284	2	US-08-655-241-20	Sequence 24, Appl
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851	6	0.8	256	2	US-09-292-411A-2	Sequence 2, Appli	924	284	2	US-09-398-326-20	Sequence 20, Appl
852	6	0.8	256	2	US-09-902-540-12724	Sequence 12724, A	925	284	2	US-09-134-000C-5638	Sequence 5638, Ap
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854	6	0.8	258	2	US-09-724-623-105	Sequence 105, App	927	285	2	US-09-540-236-2157	Sequence 2157, Ap
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856	6	0.8	258	2	US-09-081-385-150	Sequence 150, App	929	288	2	US-08-446-201-4	Sequence 4, Appli
857	6	0.8	258	2	US-09-270-767-32398	Sequence 32398, A	930	288	2	US-09-252-991A-20608	Sequence 20608, A
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861	6	0.8	258	2	US-09-712-813-150	Sequence 150, App	934	289	1	US-09-134-001C-4918	Sequence 4918, Ap
862	6	0.8	258	2	US-09-700-354A-150	Sequence 150, App	935	289	1	US-09-134-001C-3841	Sequence 3841, Ap
863	6	0.8	258	2	US-09-605-703B-450	Sequence 450, App	936	289	1	US-09-107-532A-3841	Sequence 2, Appli
864	6	0.8	258	2	US-09-605-703B-452	Sequence 452, App	937	289	1	US-08-467-852A-5	Sequence 5, Appli
865	6	0.8	259	2	US-09-270-767-45089	Sequence 45089, A	938	289	1	US-08-468-718-4	Sequence 5, Appli
866	6	0.8	259	2	US-10-320-104B-2	Sequence 2, Appli	939	289	2	US-08-247-431A-5	Sequence 5, Appli
867	6	0.8	260	2	US-09-134-001C-4009	Sequence 4009, Ap	940	289	2	US-09-543-681A-8235	Sequence 8235, Ap
868	6	0.8	260	2	US-09-489-039A-7421	Sequence 7421, Ap	941	289	2	US-09-583-110-3563	Sequence 3563, Ap
869	6	0.8	260	2	US-09-270-767-33511	Sequence 33511, A	942	290	2	US-09-634-238-236	Sequence 43846, A
870	6	0.8	260	2	US-09-270-767-46440	Sequence 46440, A	943	290	2	US-09-107-532A-3841	Sequence 2, Appli
871	6	0.8	260	2	US-09-248-796A-17592	Sequence 17592, A	944	290	2	US-09-743-847-2	Sequence 18749, A
872	6	0.8	261	2	US-09-489-039A-10725	Sequence 10725, A	945	291	2	US-09-248-796A-18749	Sequence 4458, Ap
873	6	0.8	263	2	US-09-252-991A-23754	Sequence 23754, A	946	292	2	US-09-634-238-236	Sequence 236, App
874	6	0.8	264	2	US-09-035-382-4	Sequence 4, Appli	947	292	2	US-09-270-767-43846	Sequence 43846, A
875	6	0.8	264	2	US-09-252-991A-27675	Sequence 27675, A	948	292	2	US-09-107-433-4868	Sequence 4868, Ap
876	6	0.8	264	2	US-09-134-000C-4403	Sequence 4403, Ap	949	293	2	US-09-252-991A-27745	Sequence 27745, A
877	6	0.8	264	2	US-09-902-540-16652	Sequence 16652, A	950	293	2	US-09-949-016-8027	Sequence 8027, Ap
878	6	0.8	265	2	US-10-104-047-2141	Sequence 2141, Ap	951	294	2	US-09-252-991A-26450	Sequence 26450, A
879	6	0.8	266	2	US-09-050-739-133	Sequence 153, App	952	294	2	US-09-198-452A-268	Sequence 268, App
880	6	0.8	266	2	US-09-655-908-20	Sequence 20, Appl	953	295	2	US-09-270-767-45025	Sequence 45025, A
881	6	0.8	266	2	US-09-248-796A-20084	Sequence 20084, A	954	295	2	US-09-270-767-45025	Sequence 258, App
882	6	0.8	266	2	US-09-902-540-13043	Sequence 13043, A	955	295	2	US-09-438-185A-258	Sequence 42478, A
883	6	0.8	267	2	US-09-489-039A-13450	Sequence 13450, A	956	296	2	US-09-270-767-42478	Sequence 48808, A
884	6	0.8	267	2	US-09-976-594-212	Sequence 212, App	957	297	2	US-09-270-767-48808	Sequence 14, Appl
885	6	0.8	267	2	US-09-248-796A-18561	Sequence 18561, A	958	297	2	US-09-252-991A-29778	Sequence 29778, A
886	6	0.8	267	2	US-09-902-540-14651	Sequence 14651, A	959	297	2	US-09-489-039A-10089	Sequence 10089, A
887	6	0.8	268	2	US-09-328-352-8118	Sequence 8118, Ap	960	297	2	US-10-314-639-14	Sequence 14, Appl
888	6	0.8	269	2	US-09-540-236-3336	Sequence 3336, Ap	961	298	2	US-10-059-964A-14	Sequence 6110, Ap
889	6	0.8	269	2	US-09-583-110-3865	Sequence 3865, Ap	962	298	2	US-09-543-681A-6110	Sequence 27737, A
890	6	0.8	269	2	US-09-270-767-42664	Sequence 42664, A	963	299	2	US-09-248-796A-27737	Sequence 42307, A
891	6	0.8	270	2	US-08-878-474-1	Sequence 1, Appli	964	299	2	US-09-710-279-1192	Sequence 1192, Ap
892	6	0.8	270	2	US-09-107-433-5194	Sequence 5194, Ap	965	299	2	US-09-710-279-1768	Sequence 1768, Ap
893	6	0.8	271	2	US-09-540-236-2326	Sequence 2326, Ap	966	300	2	US-09-270-767-44496	Sequence 44496, A
894	6	0.8	271	2	US-09-270-767-46455	Sequence 46455, A	967	300	2	US-09-489-039A-10251	Sequence 10251, A
895	6	0.8	271	6	5175255-1	Patent No. 5175255	968	301	2	US-09-902-540-12303	Sequence 12303, A
896	6	0.8	272	2	US-09-902-540-16810	Sequence 16810, A	969	302	2	US-08-303-861-20	Sequence 20, Appl
897	6	0.8	273	2	US-09-252-991A-25600	Sequence 25600, A	970	302	2	US-09-457-046B-24	Sequence 24, Appl
898	6	0.8	274	2	US-09-489-039A-14339	Sequence 14339, A	971	302	2	US-09-252-991A-22159	Sequence 22159, A
899	6	0.8	274	2	US-10-104-047-3353	Sequence 3353, Ap	972	302	2	US-09-107-532A-6924	Sequence 6924, Ap
900	6	0.8	276	2	US-08-961-083-134	Sequence 134, App	973	302	2	US-09-866-570B-24	Sequence 24, Appl
901	6	0.8	276	2	US-09-252-991A-17951	Sequence 17951, A	974	302	2	US-09-248-796A-15374	Sequence 15374, A
902	6	0.8	276	2	US-09-536-784-134	Sequence 134, App	975	304	2	US-09-248-796A-15270	Sequence 15270, A
903	6	0.8	276	2	US-09-902-540-15737	Sequence 15737, A	976	304	2		

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977 6 0.8 304 2 US-09-902-540-14051 Sequence 14051, A
978 6 0.8 305 2 US-09-248-796A-17837 Sequence 17837, A
979 6 0.8 305 2 US-09-248-796A-24107 Sequence 24107, A
980 6 0.8 305 2 US-09-949-016-7706 Sequence 7706, Ap
981 6 0.8 306 2 US-09-489-039A-10306 Sequence 10306, A
982 6 0.8 306 2 US-09-107-433-2663 Sequence 2663, Ap
983 6 0.8 307 2 US-09-134-001C-3792 Sequence 3792, Ap
984 6 0.8 307 2 US-09-270-767-44911 Sequence 44911, A
985 6 0.8 308 2 US-09-252-991A-27249 Sequence 27249, A
986 6 0.8 308 2 US-09-328-352-6762 Sequence 6762, Ap
987 6 0.8 309 2 US-09-270-767-44995 Sequence 44995, A
988 6 0.8 309 2 US-10-759-889-2 Sequence 2, Appl1
989 6 0.8 310 2 US-09-543-681A-6858 Sequence 6858, Ap
990 6 0.8 310 2 US-09-538-092-690 Sequence 690, App
991 6 0.8 311 2 US-09-107-532A-4438 Sequence 4438, Ap
992 6 0.8 311 2 US-09-107-532A-4439 Sequence 4439, Ap
993 6 0.8 312 2 US-09-107-433-2823 Sequence 2823, Ap
994 6 0.8 312 2 US-09-538-092-42 Sequence 42, Appl1
995 6 0.8 313 2 US-09-387-574-4 Sequence 4, Appl1
996 6 0.8 313 2 US-09-396-651B-3 Sequence 3, Appl1
997 6 0.8 313 2 US-09-668-096-4 Sequence 4, Appl1
998 6 0.8 313 2 US-09-470-512A-2 Sequence 2, Appl1
999 6 0.8 313 2 US-09-470-512A-10 Sequence 10, Appl1
1000 6 0.8 313 2 US-09-543-681A-8278 Sequence 8278, Ap
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ALIGNMENTS

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RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4
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Query Match 100.0%; Score 797; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQKIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSA 60
Db 1 MKLQKIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSA 60

Qy 61 IIKSLYATGFDDYRVETADQQLLTWIERPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120
Db 61 IIKSLYATGFDDYRVETADQQLLTWIERPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGKLNLIQTTPKVTKLARNRVDIDITDEGSAKITDIE 180
Db 121 SOYFNQATLNQAVAGLKEEYLGKLNLIQTTPKVTKLARNRVDIDITDEGSAKITDIE 180

Qy 181 PEGNQVTSDRKLMQMSLTGEGITWLTTRSNQFNQKFAQDMKVTDFYQNGYFDFRIL 240
Db 181 PEGNQVTSDRKLMQMSLTGEGITWLTTRSNQFNQKFAQDMKVTDFYQNGYFDFRIL 240

Qy 241 DTDIQTNEDEKTKOTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPGKWERQ 300
Db 241 DTDIQTNEDEKTKOTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPGKWERQ 300
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Db 241 DTDIQTNEDEKTKOTIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTWKPGKWERQ 300
Qy 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
Db 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
Qy 361 RDEVVRELRQMESAPYDTSKLORSKERVLLGYFDNVQFDVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRELRQMESAPYDTSKLORSKERVLLGYFDNVQFDVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLGAGWQDVTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDLGAGWQDVTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTA 480
Qy 481 DGVSGLDYVYGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLDYVYGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
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Db 541 YNKAPKHYADFTIKKYKGTGTGSGFKGWLKGTGVGGRNKTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPSGKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPSGKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKPRYAYPLKK 780
Db 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKPRYAYPLKK 780
Qy 781 KPEDEIQRFOFQGLGTTF 797
Db 781 KPEDEIQRFOFQGLGTTF 797

RESULT 2
US-09-994-192-2
; Sequence 2, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR FILING DATE: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2
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Best Local Similarity 100.0%; Pred. No. 3; Se-152;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTREDEVVRELRQMESAPYDTSKLORSKERV 391
Db 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTREDEVVRELRQMESAPYDTSKLORSKERV 391
Qy 392 LGYFDNVQFDVPLAGTDPKVDLNNSLTERSTGSLDLSAGWQDVTGLVMSAGVSQDNLF 451
Db 392 LGYFDNVQFDVPLAGTDPKVDLNNSLTERSTGSLDLSAGWQDVTGLVMSAGVSQDNLF 451
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QY 452 TGKSAALRASRKTTLNGSLSFDPYFTADGVSLGYD 488
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Db 452 TGKSAALRASRKTTLNGSLSFDPYFTADGVSLGYD 488

RESULT 3

US-09-489-039A-8163
; Sequence 8163, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8163
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8163

Query Match 1.0%; Score 8; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 727 SSSATGGR 734
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Db 76 SSSATGGR 83

RESULT 4

US-09-205-258-1092
; Sequence 1092, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1092
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (73)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1092

Query Match 1.0%; Score 8; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 756 SAGGAVTW 763
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Db 14 SAGGAVTW 21

RESULT 5

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; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15552
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15552

Query Match 1.0%; Score 8; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 281 KAELEKLL 288
Db 177 KAELEKLL 184

RESULT 8
US-09-252-991A-24628
; Sequence 24628, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24628
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24628

Query Match 1.0%; Score 8; DB 2; Length 648;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 VRVETADG 81
Db 94 VRVETADG 101

RESULT 9
US-09-543-681A-4998
; Sequence 4998, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4998
; LENGTH: 1589
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4998

Query Match 1.0%; Score 8; DB 2; Length 1589;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 TADQQLLL 85

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Db 563 TADGQLLL 570

RESULT 10

US-09-674-973A-147
; Sequence 147, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hydro ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 147
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-674-973A-147

Query Match 0.9%; Score 7; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 283 ELEKLLT 289

Db 5 ELEKLLT 11

RESULT 11

US-08-971-089-10
; Sequence 10, Application US/08971089
; Patent No. 6376174
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Soles, Daniel R.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,089
; FILING DATE:
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,987
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P-CE 2862
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-971-089-10

Query Match 0.9%; Score 7; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 LRASRSK 464

Db 4 LRASRSK 10

RESULT 12

US-10-117-604A-10
; Sequence 10, Application US/10117604A
; Patent No. 6960650
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Soles, Daniel R.
; TITLE OF INVENTION: Nucleic Acid Encoding
; TITLE OF INVENTION: Schwannomin-Binding-Proteins and Products Related Thereto
; FILE REFERENCE: 66783-101
; CURRENT APPLICATION NUMBER: US/10/117,604A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/030,987
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: US 08/971,089
; PRIOR FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-604A-10

Query Match 0.9%; Score 7; DB 2; Length 58;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 LRASRSK 464

Db 4 LRASRSK 10

RESULT 13

US-09-513-999C-7231
; Sequence 7231, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7231
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 51
; OTHER INFORMATION: Xaa=Ile or Leu or Val
US-09-513-999C-7231

Query Match 0.9%; Score 7; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 12, 2006, 16:19:27 ; Search time 44 Seconds
(without alignments)
1742.835 Million cell updates/sec

Title: US-10-606-618-4
Perfect score: 797
Sequence: 1 MKLKQIASALMLGISPLAF.....LKKKPEIQRFQQLGTTT 797

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.70

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_80:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	752	94.4	797	2	G81228
3	752	94.4	797	2	G81228
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5	9	1.1	435	2	T49132
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8	8	1.0	335	2	B75057
9	8	1.0	337	2	C82190
10	8	1.0	376	2	A71175
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12	8	1.0	429	2	G42365
13	8	1.0	474	1	IMBP4
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15	8	1.0	903	2	JE0327
16	8	1.0	903	2	T50334
17	8	1.0	1363	2	T43220
18	8	1.0	1577	2	A35140
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22	7	0.9	95	2	T25611
23	7	0.9	101	2	T33316
24	7	0.9	101	2	T35232
25	7	0.9	109	2	E72527
26	7	0.9	118	2	S14079
27	7	0.9	131	2	A87461
28	7	0.9	148	2	T52550
29	7	0.9	150	2	D81314
30	7	0.9	171	2	C95143
31	7	0.9	175	2	T05669
32	7	0.9	184	2	C69142
33	7	0.9	184	2	S44652
34	7	0.9	210	2	S36297
35	7	0.9	214	2	H89331
36	7	0.9	218	2	T45455
37	7	0.9	234	2	G71918
38	7	0.9	234	2	F64595
39	7	0.9	238	2	A83224
40	7	0.9	255	2	F95228
41	7	0.9	255	2	B98093
42	7	0.9	264	2	A81668
43	7	0.9	264	2	E71509
44	7	0.9	268	2	T35568
45	7	0.9	269	2	T36001
46	7	0.9	280	2	E87429
47	7	0.9	288	1	SNBYC1
48	7	0.9	305	2	A75334
49	7	0.9	305	2	T22009
50	7	0.9	306	2	T48715
51	7	0.9	306	2	AE2885
52	7	0.9	306	2	B97661
53	7	0.9	311	2	H98278
54	7	0.9	311	2	AI3004
55	7	0.9	314	2	F96574
56	7	0.9	315	2	C96802
57	7	0.9	316	2	S61237
58	7	0.9	320	1	A43824
59	7	0.9	324	2	AC0548
60	7	0.9	336	2	G84562
61	7	0.9	347	2	T06671
62	7	0.9	349	2	G97121
63	7	0.9	354	2	B89768
64	7	0.9	355	2	S29274
65	7	0.9	355	2	AC1525
66	7	0.9	359	2	T14742
67	7	0.9	363	2	S72209
68	7	0.9	366	2	C69391
69	7	0.9	373	2	S47911
70	7	0.9	377	2	A47380
71	7	0.9	380	2	AC3494
72	7	0.9	384	2	T02968
73	7	0.9	387	2	JC4578
74	7	0.9	397	1	B6BPT9
75	7	0.9	401	2	B83369
76	7	0.9	416	2	F89779
77	7	0.9	417	2	JT0950
78	7	0.9	420	2	T43932
79	7	0.9	420	2	D64492
80	7	0.9	422	1	JGAGUR
81	7	0.9	428	2	S76184
82	7	0.9	429	2	AB3574
83	7	0.9	432	2	G75199
84	7	0.9	437	1	B71233
85	7	0.9	444	2	T27866
86	7	0.9	456	2	C71226
87	7	0.9	460	2	D90084
88	7	0.9	464	2	A64974
89	7	0.9	464	2	B90989
90	7	0.9	464	2	E85834
91	7	0.9	469	2	T08310
92	7	0.9	471	2	AF1586
93	7	0.9	476	2	E57631
94	7	0.9	489	1	H70729
95	7	0.9	489	2	D95102
96	7	0.9	497	2	F97970
97	7	0.9	498	2	B90456
98	7	0.9	499	2	T34328
99	7	0.9	508	2	T20355
100	7	0.9	515	2	B90302
101	7	0.9	518	2	JC4024
102	7	0.9	518	2	F84391

hypothetical prote
hypothetical prote
hypothetical prote
f42h10.6 protein -
T-cell receptor ga
probable acetyltra
probable acyltrans
membrane fusion pr
probable ATP-bind
hypothetical prote
hypothetical prote
conserved hypochet
hypothetical prote
probable lipoprote
probable integral
conserved hypochet
proteasome endopep
lacyl-carrier-prot
hypothetical prote
hypothetical prote
transcription regu
probable transcrip
hypothetical prote
hypothetical prote
hypothetical prote
capsid protein - b
periplasmic flagel
delta-aminolevulin
hypothetical prote
hypothetical prote
gcpE protein [impo
conserved hypochet
poly (3-hydroxybut
cytochrome c oxida
hypothetical prote
3-isopropylmalate
enolase (eno) homo
PDS1 protein - Yea
RING finger-contai
oligopeptide trans
cyclin A-type (clo
recombination prot
ribonucleoside-tri
conserved hypochet
hypothetical prote
phosphoglycerate k
cell division cont
N-ethylammelne ch
lactose-binding pr
hypothetical prote
multidrug resistan
probable cell divi
hypothetical prote
hypothetical prote
hypothetical prote
RNA-polymerase sig
hypothetical prote
probable membrane
probable membrane
helicase homolog H
site-specific reco
probable membrane
cytochrome P450 Rv
hypothetical prote
site-specific DNA-
hypothetical prote
hypothetical prote
hypothetical prote
ATP-dependent RNA
poliovirus recepto
orc / cell divisio

103	7	0.9	521	2	A86909	hypothetical prote	176	6	0.8	70	2	G91236	50S ribosomal subu
104	7	0.9	526	1	KRBOVI	keratin, 54K type	177	6	0.8	70	2	G86083	50S ribosomal subu
105	7	0.9	537	2	T38015	hypothetical prote	178	6	0.8	71	2	E69345	SSU ribosomal prot
106	7	0.9	545	2	AB0290	probable membrane	179	6	0.8	72	1	B24033	small acid-soluble
107	7	0.9	562	2	S61295	heat shock protein	180	6	0.8	74	2	AI0349	conserved hypotet
108	7	0.9	564	2	H82319	conserved hypotet	181	6	0.8	74	2	AI0371	hypothetical prote
109	7	0.9	587	2	JC5300	Ran GTPase activat	182	6	0.8	76	2	A48784	Ig kappa V regions
110	7	0.9	589	2	T52070	RNAL protein homol	183	6	0.8	76	2	B88318	protein age-1 limp
111	7	0.9	589	2	A36983	RNAL homolog fagl	184	6	0.8	76	2	F70241	hypothetical prote
112	7	0.9	619	2	S40938	hypothetical prote	185	6	0.8	77	2	AC2101	lipoprotein [impor
113	7	0.9	620	2	S38994	origin recognition	186	6	0.8	78	2	AC4450	ribosomal protein
114	7	0.9	623	2	AD2295	hypothetical prote	187	6	0.8	78	2	AF2345	hypothetical prote
115	7	0.9	625	2	A72592	glutamine-fructose	188	6	0.8	79	2	S68245	phosphatidylcholin
116	7	0.9	649	1	H64476	lipoteate protein li	189	6	0.8	79	2	F70013	hypothetical prote
117	7	0.9	656	2	H84649	probable DnaJ prot	190	6	0.8	80	2	G81108	hypothetical prote
118	7	0.9	666	2	D82386	methyl-accepting c	191	6	0.8	80	2	A32364	photosystem I iron
119	7	0.9	728	2	S71467	diacylglycerol kin	192	6	0.8	80	2	G97805	hypothetical prote
120	7	0.9	745	2	D96829	homeobox protein (193	6	0.8	81	1	FEPM15	photosystem I iron
121	7	0.9	747	2	S71478	homeotic protein A	194	6	0.8	81	1	FERZA	photosystem I iron
122	7	0.9	771	2	T01315	hypothetical prote	195	6	0.8	81	1	FEWT1	photosystem I iron
123	7	0.9	784	2	E82731	outer membrane ant	196	6	0.8	81	1	FEZM1C	photosystem I iron
124	7	0.9	797	2	H83190	probable outer mem	197	6	0.8	81	2	S07170	photosystem I iron
125	7	0.9	812	2	HA1049	ribonuclease R (RN	198	6	0.8	81	2	S73295	photosystem I iron
126	7	0.9	823	2	T52425	kinesin-like prote	199	6	0.8	81	2	T07571	photosystem I iron
127	7	0.9	827	1	S56404	virulence-associat	200	6	0.8	81	2	S12198	photosystem I iron
128	7	0.9	827	2	C86114	probable enzyme va	201	6	0.8	81	2	AI3461	hypothetical prote
129	7	0.9	827	2	C91273	probable enzyme [i	202	6	0.8	81	2	A98247	hypothetical prote
130	7	0.9	856	2	F96998	phosphoenolpyruvat	203	6	0.8	81	2	H97567	hypothetical prote
131	7	0.9	881	2	I84737	kinesin heavy chai	204	6	0.8	83	2	F81267	30S ribosomal prot
132	7	0.9	888	2	D96619	protein T30E16.9 [205	6	0.8	83	2	S77417	protochlorophyllid
133	7	0.9	942	2	T19553	hypothetical prote	206	6	0.8	83	2	AI0032	probable type III
134	7	0.9	953	1	B30169	leukotoxin A - Pas	207	6	0.8	84	2	E97807	hypothetical prote
135	7	0.9	963	1	A41919	kinesin heavy chai	208	6	0.8	85	2	T08595	cysteine proteinas
136	7	0.9	983	2	AG2381	glycine cleavage s	209	6	0.8	85	2	AI0316	sec-independent pr
137	7	0.9	1054	2	D70425	conserved hypotet	210	6	0.8	86	2	H85939	type III secretion
138	7	0.9	1088	2	A69493	cysteine proteinas	211	6	0.8	86	2	D91094	type III secretion
139	7	0.9	1121	2	JC7329	WD-repeat protein	212	6	0.8	86	2	QJ0730	9K protein - prote
140	7	0.9	1221	2	T25005	hypothetical prote	213	6	0.8	86	2	E82985	hypothetical prote
141	7	0.9	1222	2	B90593	hypothetical prote	214	6	0.8	86	2	AG3442	helix-turn-helix p
142	7	0.9	1234	2	T31623	hypothetical prote	215	6	0.8	87	2	T05709	auxin-induced prot
143	7	0.9	1259	2	T32901	hypothetical prote	216	6	0.8	88	2	C82468	hypothetical prote
144	7	0.9	1366	2	C85077	probable polyprote	217	6	0.8	88	2	E70880	hypothetical prote
145	7	0.9	1434	2	T30172	transmembrane prot	218	6	0.8	90	2	S15149	hypothetical prote
146	7	0.9	1442	2	T18538	patched protein -	219	6	0.8	90	2	B82799	hypothetical prote
147	7	0.9	1449	2	B81963	IgA-specific serin	220	6	0.8	91	2	S17627	Ig kappa chain V r
148	7	0.9	1457	2	D81019	adhesion and penet	221	6	0.8	91	2	S17629	Ig kappa chain V r
149	7	0.9	1513	2	T44045	hypothetical prote	222	6	0.8	91	2	S17638	Ig kappa chain V r
150	7	0.9	1520	2	T44231	hypothetical prote	223	6	0.8	91	2	S17639	Ig kappa chain V r
151	7	0.9	1658	2	D75489	hypothetical prote	224	6	0.8	91	2	S17628	Ig kappa chain V r
152	7	0.9	1943	2	B64596	toxin-like outer m	225	6	0.8	91	2	S17637	Ig kappa chain V r
153	7	0.9	2174	2	E95965	hypothetical glyci	226	6	0.8	93	2	B69190	hypothetical prote
154	7	0.9	2274	2	T30258	adenomatous polypo	227	6	0.8	93	2	G71370	probable ribosomal
155	7	0.9	2431	1	MNVVSF	nonstructural poly	228	6	0.8	93	2	D70192	chaperonin (groES)
156	7	0.9	2478	2	AH2140	polyketide synthas	229	6	0.8	94	2	A60097	cortical cytokele
157	7	0.9	3194	2	D71917	toxin-like outer m	230	6	0.8	94	2	S32105	chaperonin groES -
158	7	0.9	4385	2	T29042	hypothetical prote	231	6	0.8	94	2	JN0660	heat shock protein
159	7	0.9	4485	2	T08044	dynein gamma heavy	232	6	0.8	94	2	B40506	PRF2 protein - hum
160	7	0.9	5369	2	T44807	mycosubtilin synth	233	6	0.8	94	2	S75365	hypothetical prote
161	6	0.8	17	2	I55612	thyroid hormone re	234	6	0.8	95	2	D33730	Ig kappa chain V r
162	6	0.8	23	2	S45030	homeotic protein S	235	6	0.8	95	2	T03068	hypothetical prote
163	6	0.8	23	2	S60569	homeodomain protei	236	6	0.8	96	2	B26074	cysteine proteinas
164	6	0.8	25	2	D41606	homeotic protein M	237	6	0.8	96	2	S34937	heat shock protein
165	6	0.8	52	2	A12399	hypothetical prote	238	6	0.8	96	2	C82048	chaperonin, 10 Kd
166	6	0.8	57	2	AB0373	hypothetical prote	239	6	0.8	96	2	JC4518	hypothetical prote
167	6	0.8	62	2	F75338	hypothetical prote	240	6	0.8	96	2	H97048	Ig light chain V r
168	6	0.8	62	2	G70988	hypothetical prote	241	6	0.8	97	2	S26341	Ig light chain V r
169	6	0.8	65	2	H82773	hypothetical prote	242	6	0.8	97	2	PH1084	Ig light chain V r
170	6	0.8	66	2	AF3083	hypothetical prote	243	6	0.8	97	2	F84029	hypothetical prote
171	6	0.8	67	2	F85904	hypothetical prote	244	6	0.8	98	2	B82416	hypothetical prote
172	6	0.8	68	2	H90086	hypothetical prote	245	6	0.8	98	2	H82577	hypothetical prote
173	6	0.8	68	2	F84002	hypothetical prote	246	6	0.8	99	2	S51210	Ig kappa chain V r
174	6	0.8	69	2	S33899	ribosomal protein	247	6	0.8	99	2	S53124	probable ribosomal
175	6	0.8	70	1	R5EC31	ribosomal protein	248	6	0.8	100	2	S29590	Ig kappa chain V r

249	6	0.8	100	2	S03636	homeotic protein H	322	6	0.8	126	2	D95410	hypothetical prote
250	6	0.8	101	2	F82421	conserved hypotet	323	6	0.8	127	2	F75092	ssu ribosomal prot
251	6	0.8	101	2	C69076	hypothetical prote	324	6	0.8	127	2	D97381	methylglyoxal synt
252	6	0.8	102	2	S11115	ig kappa chain v r	325	6	0.8	127	2	AC2599	methylglyoxal synt
253	6	0.8	102	2	AF3346	SSU ribosomal prot	326	6	0.8	127	2	S75086	translation initia
254	6	0.8	102	2	H87403	ribosomal protein	327	6	0.8	128	2	S36678	ywbH protein - Bac
255	6	0.8	102	2	A23931	anti-lipoplysacch	328	6	0.8	128	2	F84216	hypothetical prote
256	6	0.8	103	2	S29591	ig kappa chain v r	329	6	0.8	128	2	S53584	probable membrane
257	6	0.8	103	2	G75257	hypothetical prote	330	6	0.8	129	2	B72853	AcOrf-26 protein -
258	6	0.8	104	2	B49049	ig kappa chain v r	331	6	0.8	129	2	T41771	AcMNPV orf26 - Bom
259	6	0.8	105	2	D95108	conserved hypotet	332	6	0.8	129	2	T46300	hypothetical prote
260	6	0.8	106	2	P50071	ig kappa chain v r	333	6	0.8	129	2	S45868	probable membrane
261	6	0.8	106	2	S11114	ig kappa chain v r	334	6	0.8	129	2	T36916	hypothetical prote
262	6	0.8	106	2	S11120	ig kappa chain v r	335	6	0.8	130	1	JL0079	ig kappa chain pre
263	6	0.8	106	2	G72059	conserved hypotet	336	6	0.8	130	1	JL0079	chorion class B pr
264	6	0.8	106	2	D86563	hypothetical prote	337	6	0.8	130	2	S01439	lens fiber membran
265	6	0.8	106	2	T24774	hypothetical prote	338	6	0.8	130	2	S01439	hypothetical prote
266	6	0.8	106	2	G27887	ig kappa chain v r	339	6	0.8	130	2	H83150	hypothetical prote
267	6	0.8	107	1	PXPSEP	putidaredoxin [val	340	6	0.8	131	1	SI2972	anicyanin - Paraco
268	6	0.8	107	1	B36950	urease (EC 3.5.1.5	341	6	0.8	131	2	C87416	Mut7/nudix family
269	6	0.8	107	2	S11112	ig kappa chain v r	342	6	0.8	131	2	B71055	hypothetical prote
270	6	0.8	107	2	S11118	ig kappa chain v r	343	6	0.8	132	2	C70161	ribosomal protein
271	6	0.8	107	2	S11116	ig kappa chain v r	344	6	0.8	132	2	D72583	hypothetical prote
272	6	0.8	107	2	P00111	ig kappa chain v r	345	6	0.8	132	2	S39540	homeotic protein G
273	6	0.8	107	2	S11113	ig kappa chain v r	346	6	0.8	133	2	T01042	hypothetical prote
274	6	0.8	107	2	P03395	ig kappa chain v r	347	6	0.8	134	2	C69849	hypothetical prote
275	6	0.8	107	2	P04002	ig kappa chain v r	348	6	0.8	135	2	AF2055	hypothetical prote
276	6	0.8	107	2	S11119	ig kappa chain v r	349	6	0.8	135	2	B72768	hypothetical prote
277	6	0.8	107	2	P03397	ig kappa chain v r	350	6	0.8	136	2	T49582	positive regulatio
278	6	0.8	107	2	S11123	ig kappa chain v r	351	6	0.8	136	2	S04043	hypothetical prote
279	6	0.8	107	2	P03398	ig kappa chain v r	352	6	0.8	137	2	T45079	hypothetical prote
280	6	0.8	107	2	S11121	ig kappa chain v r	353	6	0.8	138	1	A69219	hypothetical prote
281	6	0.8	107	2	S11117	ig kappa chain v r	354	6	0.8	138	2	B83135	hypothetical prote
282	6	0.8	107	2	A30562	ig kappa chain v r	355	6	0.8	139	2	G85906	hypothetical prote
283	6	0.8	107	2	P04006	ig kappa chain v r	356	6	0.8	139	2	H97449	probable isomerase
284	6	0.8	107	2	P03562	ig kappa chain v r	357	6	0.8	139	2	S32510	homeobox-contains
285	6	0.8	107	2	P04405	ig kappa chain v r	358	6	0.8	140	2	E97462	organic hydroperox
286	6	0.8	107	2	T17701	hypothetical prote	359	6	0.8	140	2	AG2680	hemoglobin alpha-I
287	6	0.8	108	2	C48078	biliary glycoprote	360	6	0.8	141	1	HALZC	kinesin heavy chai
288	6	0.8	108	2	G30560	ig kappa chain v r	361	6	0.8	143	2	C44259	hypothetical prote
289	6	0.8	109	2	C30515	ig heavy chain v r	362	6	0.8	143	2	A69115	DNA transport mach
290	6	0.8	109	2	D91085	hypothetical prote	363	6	0.8	143	2	E30338	transposase IS240-
291	6	0.8	109	2	F85930	hypothetical prote	364	6	0.8	143	2	B69267	trypanothione-glut
292	6	0.8	109	2	D65061	hypothetical prote	365	6	0.8	143	2	S58429	conserved hypotet
293	6	0.8	109	2	AH3240	conserved hypotet	366	6	0.8	143	2	AG2682	hypothetical prote
294	6	0.8	110	2	S13383	probable membrane	367	6	0.8	143	2	E97464	probable Sdhb subu
295	6	0.8	111	2	G85974	suppressor protein	368	6	0.8	144	2	C72668	hypothetical prote
296	6	0.8	111	2	G91129	genome polyprotein	369	6	0.8	145	2	D70843	hypothetical prote
297	6	0.8	112	2	S51121	polyprotein - hepa	370	6	0.8	145	2	T36527	major tail shaft p
298	6	0.8	113	2	P02774	polyprotein - hepa	371	6	0.8	145	2	AD1447	heat shock protein
299	6	0.8	113	2	P02773	xis 5'-region hypo	372	6	0.8	145	2	F69214	conserved hypotet
300	6	0.8	113	2	A55205	transcription fact	373	6	0.8	145	2	F90185	hypothetical prote
301	6	0.8	113	2	I51025	conserved hypotet	374	6	0.8	145	2	S26443	calmodulin-like pr
302	6	0.8	114	2	E97976	hypothetical prote	375	6	0.8	146	2	T51473	hypothetical prote
303	6	0.8	115	2	T29883	hypothetical prote	376	6	0.8	146	2	T22474	hypothetical prote
304	6	0.8	117	2	H71431	hypothetical prote	377	6	0.8	146	2	H64126	conserved hypotet
305	6	0.8	117	2	T13096	probable minor cap	378	6	0.8	146	2	B82167	conserved hypotet
306	6	0.8	117	2	S75884	hypothetical prote	379	6	0.8	146	2	AE2935	hypothetical prote
307	6	0.8	119	2	A64249	ribosomal protein	380	6	0.8	146	2	B98347	ig heavy chain pre
308	6	0.8	119	2	B84407	hypothetical prote	381	6	0.8	146	2	PH0127	ig heavy chain pre
309	6	0.8	120	2	S22049	reverse transcript	382	6	0.8	147	2	PH0131	ig heavy chain pre
310	6	0.8	120	2	AB2668	conserved hypotet	383	6	0.8	147	2	PH0123	ig heavy chain pre
311	6	0.8	120	2	AH1813	hypothetical prote	384	6	0.8	147	2	PH0125	ig heavy chain pre
312	6	0.8	121	2	H70471	conserved hypotet	385	6	0.8	147	2	PH0124	ig heavy chain pre
313	6	0.8	122	2	F97779	hypothetical prote	386	6	0.8	147	2	PH0130	ig heavy chain pre
314	6	0.8	123	2	G71189	hypothetical prote	387	6	0.8	147	2	PH0130	myosin calcium-bin
315	6	0.8	124	2	F82205	chemotaxis protein	388	6	0.8	147	2	A29910	hypothetical prote
316	6	0.8	124	2	G75172	hypothetical prote	389	6	0.8	147	2	T28131	hypothetical prote
317	6	0.8	124	2	AD3428	transposase BMEI14	390	6	0.8	150	2	A97536	hypothetical prote
318	6	0.8	124	2	S05005	homeotic protein H	391	6	0.8	151	2	T15428	hypothetical prote
319	6	0.8	125	2	C82831	ribosomal-binding	392	6	0.8	151	2	A75297	hypothetical prote
320	6	0.8	125	2	AC3195	hypothetical prote	393	6	0.8	152	2	S29752	ubiquitin-activati
321	6	0.8	125	2	T16848	hypothetical prote	394	6	0.8	153	1	JT0572	profilin - Tetrah

395	6	0.8	153	1	WRBP15	early protein gp17	468	6	0.8	178	2	A47071	hypothetical prote
396	6	0.8	153	1	G69847	conserved hypotet	469	6	0.8	179	2	A53522	pepidylprolyl iso
397	6	0.8	153	2	S63367	ribosomal protein	470	6	0.8	179	2	B65695	ribosomal protein
398	6	0.8	153	2	AH2203	bacterioferritin c	471	6	0.8	179	2	T48416	hypothetical prote
399	6	0.8	153	2	G70077	hypothetical prote	472	6	0.8	181	2	AD2427	hypothetical prote
400	6	0.8	153	2	S34255	hypothetical prote	473	6	0.8	181	2	E83436	probable oxidase P
401	6	0.8	153	2	C86324	protein F14D16.23	474	6	0.8	182	2	A02947	keratin, 60K type
402	6	0.8	154	2	H70581	hypothetical prote	475	6	0.8	182	2	A91031	probable fimbrial-
403	6	0.8	154	2	T34821	hypothetical prote	476	6	0.8	182	2	AH1579	hypothetical prote
404	6	0.8	155	2	T15379	hypothetical prote	477	6	0.8	182	2	G90235	hypothetical prote
405	6	0.8	156	2	F84356	hypothetical prote	478	6	0.8	183	2	A40360	hypothetical prote
406	6	0.8	156	2	AG0243	probable exported	479	6	0.8	183	2	C85786	hypothetical prote
407	6	0.8	157	2	F82390	methylated-DNA-[pr	480	6	0.8	183	2	G90937	hypothetical prote
408	6	0.8	159	2	D72886	hypothetical prote	481	6	0.8	183	2	S26961	H+-transporting tw
409	6	0.8	160	2	T11949	hypothetical prote	482	6	0.8	183	2	T37965	probable 40S ribos
410	6	0.8	161	2	JC1751	vacuolar H+-ATPase	483	6	0.8	183	2	B90092	hypothetical prote
411	6	0.8	161	2	F71860	biotin carboxyl ca	484	6	0.8	184	2	A05045	hypothetical prote
412	6	0.8	161	2	G71407	transcription fact	485	6	0.8	184	2	T33006	hypothetical prote
413	6	0.8	161	2	S50931	hypothetical prote	486	6	0.8	184	2	B71897	hypothetical prote
414	6	0.8	162	1	RPMWA	phycoerythrocyanin	487	6	0.8	185	2	G75379	conserved hypotet
415	6	0.8	162	2	H70314	hypothetical prote	488	6	0.8	185	2	A13454	hypothetical prote
416	6	0.8	164	1	D69783	transcription regu	489	6	0.8	185	2	T19073	probable pyruvate
417	6	0.8	164	2	AE1900	NADH dehydrogenase	490	6	0.8	186	2	T19073	hypothetical prote
418	6	0.8	165	2	D97283	ribosomal protein	491	6	0.8	186	2	AF3094	hypothetical prote
419	6	0.8	165	2	B72618	hypothetical prote	492	6	0.8	186	2	F90646	probable fimbrial
420	6	0.8	165	2	AG2428	hypothetical prote	493	6	0.8	186	2	F85497	probable fimbrial
421	6	0.8	166	2	G78003	cuticle structural	494	6	0.8	187	2	H95998	probable drpp-4-de
422	6	0.8	166	2	G90661	probable peptide c	495	6	0.8	187	2	D99192	hypothetical prote
423	6	0.8	166	2	B85512	translation releas	496	6	0.8	188	2	JU0451	hypothetical 21K p
424	6	0.8	166	2	E64748	translation releas	497	6	0.8	188	2	I59116	myc protein - huma
425	6	0.8	167	2	C71803	ubiquinol-cytochro	498	6	0.8	188	2	I79500	myc protein - huma
426	6	0.8	167	2	JW0065	fast skeletal trop	499	6	0.8	188	2	C97438	hypothetical prote
427	6	0.8	167	2	S07473	early light-induce	500	6	0.8	188	2	AF2656	conserved hypotet
428	6	0.8	167	2	AC0481	probable gluconoki	501	6	0.8	189	2	E96569	probable IAA6 prot
429	6	0.8	167	2	D55224	hypothetical prote	502	6	0.8	189	2	S58493	auxin-induced prot
430	6	0.8	167	2	G90175	NADH dehydrogenase	503	6	0.8	189	2	S70104	hypothetical prote
431	6	0.8	168	2	S41973	serine proteinase	504	6	0.8	190	2	AD3329	acetolactate synth
432	6	0.8	169	1	WQECF3	phosphotransferase	505	6	0.8	191	1	JH0585	ribosomal protein
433	6	0.8	169	1	H69136	hypothetical prote	506	6	0.8	191	2	B64597	adenylate kinase -
434	6	0.8	169	2	D85884	PTS system, glucos	507	6	0.8	191	2	C90518	recombination prot
435	6	0.8	169	2	A98040	glucose-specific P	508	6	0.8	191	2	H64887	probable phage-rel
436	6	0.8	169	2	T44852	molybdopterin co-f	509	6	0.8	191	2	E64909	probable phage-rel
437	6	0.8	169	2	I51903	type I interleukin	510	6	0.8	191	2	E72455	hypothetical prote
438	6	0.8	169	2	C70207	outer membrane pro	511	6	0.8	191	2	S74679	hypothetical prote
439	6	0.8	170	2	C75184	VPS29-like phospho	512	6	0.8	191	2	I40153	outer surface prot
440	6	0.8	170	2	S53648	ribosomal protein	513	6	0.8	191	2	E84375	hypothetical prote
441	6	0.8	170	2	F87482	hypothetical prote	514	6	0.8	191	2	A64704	hypothetical prote
442	6	0.8	171	1	JBA041	chorion class B pr	515	6	0.8	191	2	A71814	hypothetical prote
443	6	0.8	171	2	G70883	probable lppU prot	516	6	0.8	192	2	S70267	outer surface prot
444	6	0.8	171	2	E87459	cytochrome c famil	517	6	0.8	192	2	T05159	hypothetical prote
445	6	0.8	172	2	B81897	probable host-nucl	518	6	0.8	193	2	E85693	probable tail fibre
446	6	0.8	172	2	S07474	early light-induce	519	6	0.8	193	2	C90835	tail fiber assembl
447	6	0.8	172	2	B83696	hypothetical prote	520	6	0.8	193	2	D81009	conserved hypotet
448	6	0.8	173	2	D90177	1S0 ribosomal prot	521	6	0.8	193	2	E82031	probable integral
449	6	0.8	173	2	B85875	probable minor fim	522	6	0.8	193	2	S70276	outer surface prot
450	6	0.8	173	2	A70914	hypothetical prote	523	6	0.8	193	2	S70287	outer surface prot
451	6	0.8	174	2	B75176	hypothetical prote	524	6	0.8	194	1	R5PM24	ribosomal protein
452	6	0.8	174	2	T03056	hypothetical prote	525	6	0.8	194	2	T16556	hypothetical prote
453	6	0.8	174	2	T27552	hypothetical prote	526	6	0.8	194	2	T52044	dof zinc finger pr
454	6	0.8	174	2	D86239	protein T10024.23	527	6	0.8	194	2	T20277	outer surface prot
455	6	0.8	175	2	JC7274	DNA binding protei	528	6	0.8	194	2	T20322	hypothetical prote
456	6	0.8	175	2	C39141	transcription repr	529	6	0.8	195	2	AE1823	hypothetical prote
457	6	0.8	175	2	A82297	conserved hypotet	530	6	0.8	195	2	G83170	hypothetical prote
458	6	0.8	176	2	AD1174	conserved hypotet	531	6	0.8	196	2	B86653	hypothetical prote
459	6	0.8	176	2	AE1531	conserved hypotet	532	6	0.8	196	2	C64891	ferriphycoelin-bin
460	6	0.8	177	2	F83114	50S ribosomal prot	533	6	0.8	196	2	AH2441	hypothetical prote
461	6	0.8	178	2	G91182	probable fimbrial	534	6	0.8	196	2	G97964	conserved hypotet
462	6	0.8	178	2	C86029	probable major fim	535	6	0.8	196	2	AB1601	dtcdp-glucose 4-6-d
463	6	0.8	178	2	B95183	non-heme iron-cont	536	6	0.8	197	2	JC3239	neutrophil gelatin
464	6	0.8	178	2	E98050	hypothetical prote	537	6	0.8	198	2	S72709	lepb170_C3_229 pr
465	6	0.8	178	2	T01890	hypothetical prote	538	6	0.8	198	2	A25706	sorcin - Chinese h
466	6	0.8	178	2	I40104	outer surface prot	539	6	0.8	198	2	S52094	sorcin - human
467	6	0.8	178	2	I40125	outer surface prot	540	6	0.8	199	2	C96570	hypothetical prote

541	6	0.8	200	2	B96912	adenylylsulfate ki	614	221	2	A72097	probable ABC trans
542	6	0.8	200	2	S07397	lipocalin - mouse	615	221	2	G86525	probable ABC trans
543	6	0.8	200	2	S10946	transcription init	616	221	2	T15999	hypothetical prote
544	6	0.8	200	2	S10945	transcription init	617	222	2	T72572	probable TATA-box
545	6	0.8	200	2	AB1085	hypothetical prote	618	222	2	H82794	hypothetical prote
546	6	0.8	201	2	T38262	hypothetical prote	619	222	2	G87380	hypothetical prote
547	6	0.8	201	2	T49121	receptor like prot	620	222	2	S62001	WE15 protein - yea
548	6	0.8	201	2	G85253	probable two-compo	621	222	2	A84436	probable glutathio
549	6	0.8	202	2	T35545	probable two-compo	622	223	2	T36952	conserved hypoteth
550	6	0.8	202	2	T46515	hypothetical prote	623	223	2	S73367	hypothetical prote
551	6	0.8	202	2	C90034	hypothetical prote	624	223	2	B89567	protein T08A9.9 [i
552	6	0.8	202	2	T47319	hypothetical prote	625	224	2	AG1196	ribose 5-phosphate
553	6	0.8	203	2	G86785	acetyltransferase	626	224	2	S31845	chlorophyll a/b-bi
554	6	0.8	203	2	C97766	holiday junction	627	225	1	SYECDB	dethiobiotin synth
555	6	0.8	203	2	B72566	hypothetical prote	628	225	2	A99206	hypothetical prote
556	6	0.8	203	2	AH0223	probable glycosida	629	225	2	AH3080	RhtB family transp
557	6	0.8	203	2	S35563	sex-determining pr	630	226	2	G87518	lipote-protein li
558	6	0.8	204	2	S27526	5-bromo-4-chloroin	631	226	2	S23280	homeotic protein m
559	6	0.8	204	2	A10542	probable peptide c	632	226	2	1 ADMSC	fructose-bisphosph
560	6	0.8	205	2	D90455	hypothetical prote	633	227	2	A38452	2-haloacid dehalog
561	6	0.8	206	2	A10700	probable two-compo	634	227	2	T49711	hypothetical prote
562	6	0.8	206	2	AC2443	orotate phosphorib	635	227	2	B82408	ABC transporter, A
563	6	0.8	206	2	C82139	conserved hypoteth	636	228	2	T37026	probable lipoprote
564	6	0.8	207	2	G71053	hypothetical prote	637	228	2	C90276	conserved hypoteth
565	6	0.8	208	1	A42045	glutathione transf	638	230	2	T34822	ABC-transporter AT
566	6	0.8	208	1	S29543	interleukin-6 - sh	639	230	2	C64396	precorrin-2 methyl
567	6	0.8	208	2	C84657	2-dehydro-3-deoxy-	640	230	2	E71224	probable HESA prot
568	6	0.8	208	2	D71859	glutathione transf	641	231	2	E71224	hypothetical prote
569	6	0.8	209	1	XUFF11	outer surface prot	642	231	2	AE2297	hypothetical prote
570	6	0.8	209	2	I40142	hypothetical prote	643	232	2	S75699	cAMP receptor prot
571	6	0.8	209	2	D66882	DNA-directed DNA p	644	232	2	H72807	gp65 protein - Myc
572	6	0.8	210	1	JN0277	probable 2-dehydro	645	232	2	S15960	hypothetical prote
573	6	0.8	210	2	F71308	imidazoleglycerol-	646	233	2	T28914	hypothetical prote
574	6	0.8	210	2	JC4381	transcription regu	647	233	2	T06995	probable MADS box
575	6	0.8	210	2	T06864	probable acetyltra	648	234	2	H81669	conserved hypoteth
576	6	0.8	210	2	H75599	hypothetical prote	649	234	2	T20933	hypothetical prote
577	6	0.8	210	2	T26154	hypothetical prote	650	235	2	B69814	ig kappa chain - m
578	6	0.8	210	2	I58391	sarcoma amplified	651	235	2	S25058	hypothetical prote
579	6	0.8	211	1	E71262	VPS29-like phospho	652	235	2	T36923	coat protein - pot
580	6	0.8	211	2	H64216	ribosomal protein	653	236	2	S16164	coat protein - pot
581	6	0.8	211	2	B89830	hypothetical prote	654	236	2	S35766	coat protein - pot
582	6	0.8	211	2	T49930	hypothetical prote	655	236	2	S41326	coat protein - pot
583	6	0.8	212	2	T44591	hypothetical prote	656	236	2	JQ2298	coat protein - pot
584	6	0.8	213	2	E71511	hypothetical prote	657	237	2	C84065	transcription regu
585	6	0.8	213	2	E72548	hypothetical prote	658	237	2	S47351	p30 B3.10 protein
586	6	0.8	213	2	A95863	hypothetical prote	659	237	2	A97336	Na+ ABC transporter
587	6	0.8	214	2	AB2195	serine esterase [i	660	238	2	AI0077	conserved hypoteth
588	6	0.8	214	2	T51657	myb-related transc	661	239	2	A75293	amino acid ABC tra
589	6	0.8	214	2	A97540	hypothetical prote	662	239	2	T51534	hypothetical prote
590	6	0.8	214	2	AC2759	cytochrome b561 At	663	240	2	S75021	3-ketoacyl-acyl ca
591	6	0.8	215	2	A71541	hypothetical prote	664	240	2	H90778	DNA-binding protei
592	6	0.8	216	2	D75567	GTP cyclohydrolase	665	241	2	T00751	probable protein k
593	6	0.8	216	2	A12635	two component resp	666	242	2	H69885	3-oxoacyl-acyl-ca
594	6	0.8	216	2	D86564	yagB family [impor	667	242	2	C85640	hypothetical prote
595	6	0.8	216	2	G72060	yagE family - Chla	668	242	2	G87696	homeotic protein G
596	6	0.8	216	2	S58100	ribosomal protein	669	242	2	A43904	probable phosphoes
597	6	0.8	216	2	F71378	hypothetical prote	670	243	1	B86746	hypothetical prote
598	6	0.8	216	2	C84900	hypothetical prote	671	243	2	B71512	mip protein - Legi
599	6	0.8	217	1	KIBSAF	adenylate kinase (672	243	2	A43596	hypothetical prote
600	6	0.8	217	2	T16518	hypothetical prote	673	243	2	A69225	GBX1 protein - chi
601	6	0.8	218	2	F84170	hypothetical prote	674	243	2	JC7596	phosphoadenyl-su
602	6	0.8	218	2	T01076	transcription fact	675	244	1	RDECPA	hypothetical prote
603	6	0.8	219	2	B82727	2-keto-3-deoxy-6-p	676	244	2	B64003	conserved hypoteth
604	6	0.8	219	2	S52646	GTP-binding protei	677	244	2	B89381	NADH dehydrogenase
605	6	0.8	219	2	T09720	conserved hypoteth	678	245	2	AB2286	hypothetical prote
606	6	0.8	219	2	T33190	hypothetical prote	679	245	2	B86738	transcription regu
607	6	0.8	220	2	T51827	MADS-box Protein [680	246	2	AC3024	hypothetical prote
608	6	0.8	220	2	T05580	MADS-box protein A	681	246	2	T00704	hypothetical prote
609	6	0.8	220	2	D85991	probable transcrip	682	247	2	S74961	conserved hypoteth
610	6	0.8	220	2	B65119	potential acraf/en	683	247	2	G83382	hypothetical prote
611	6	0.8	220	2	H91145	probable transcrip	684	247	2	D89453	conserved hypoteth
612	6	0.8	220	2	T15275	hypothetical prote	685	248	2	F64788	hypothetical prote
613	6	0.8	220	2	T12474	hypothetical prote	686	248	2	F69449	tryptophan synthas

687	6	0.8	248	2	I64230	sensory rhodopsin	760	6	0.8	266	2	T25230	hypothetical prote
688	6	0.8	249	1	A30113	NADH2 dehydrogenas	761	6	0.8	266	2	T22185	hypothetical prote
689	6	0.8	249	1	B30113	NADH2 dehydrogenas	762	6	0.8	267	2	H86320	probable MYB47 tra
690	6	0.8	249	2	AF1405	creatine amido-hy	763	6	0.8	267	2	E64175	hypothetical prote
691	6	0.8	249	2	AF1781	creatine amido-hy	764	6	0.8	267	2	E83232	probable ATP-bind
692	6	0.8	250	2	H95161	conserved hypochet	765	6	0.8	267	2	S74998	hypothetical prote
693	6	0.8	250	2	G98027	conserved hypochet	766	6	0.8	267	2	E75471	transcription regu
694	6	0.8	250	2	G72650	hypothetical prote	767	6	0.8	267	2	A46122	homeotic protein H
695	6	0.8	250	2	D75119	hypothetical prote	768	6	0.8	267	2	A49068	cranosynotosis-as
696	6	0.8	251	2	I57668	luteinizing hormon	769	6	0.8	268	1	A49473	glutamate racemase
697	6	0.8	251	2	H65007	VacJ lipoprotein p	770	6	0.8	268	2	S31010	gene 65 protein -
698	6	0.8	251	2	E91032	lipoprotein precur	771	6	0.8	268	2	A46980	hypothetical prote
699	6	0.8	251	2	F85876	lipoprotein precur	772	6	0.8	268	2	AE0241	conserved hypochet
700	6	0.8	251	2	F70412	dihydroorotate deh	773	6	0.8	268	2	S18814	homeotic protein H
701	6	0.8	252	2	C95183	triosephosphate is	774	6	0.8	269	2	T16115	hypothetical prote
702	6	0.8	252	2	A28449	tropomyosin, cytos	775	6	0.8	269	2	B84013	hypothetical prote
703	6	0.8	252	2	T10697	immature seed prot	776	6	0.8	269	2	T26504	hypothetical prote
704	6	0.8	253	2	H69219	pyroline-5-carbox	777	6	0.8	270	1	CCECID	cell division inhi
705	6	0.8	253	2	JQ2255	triose-phosphate i	778	6	0.8	270	2	B84968	septum site-determ
706	6	0.8	253	2	S44053	structural protein	779	6	0.8	270	2	AH0724	septum site-determ
707	6	0.8	253	2	F69134	hypothetical prote	780	6	0.8	270	2	F85695	cell division inhi
708	6	0.8	253	2	G81311	probable ATP/GTP-b	781	6	0.8	270	2	E90837	cell division inhi
709	6	0.8	253	2	AI3598	transposase BMSII0	782	6	0.8	270	2	AE0253	septum site-determ
710	6	0.8	254	2	B87396	DNA-binding respon	783	6	0.8	270	2	S71793	head-inducing fact
711	6	0.8	254	2	T08476	inclusion membrane	784	6	0.8	270	2	C81230	septum site-determ
712	6	0.8	254	2	E84382	hypothetical prote	785	6	0.8	271	2	JQ0950	ICP 18.5 protein -
713	6	0.8	254	2	C81208	ABC transporter, A	786	6	0.8	271	2	B60176	hypothetical prote
714	6	0.8	254	2	H81784	probable ABC trans	787	6	0.8	272	2	C75548	hypothetical prote
715	6	0.8	255	1	I5ECT	triose-phosphate i	788	6	0.8	273	2	AH2709	transcription regu
716	6	0.8	255	2	A35255	chlorocatechol 1,2	789	6	0.8	273	2	S12637	transposase - Esch
717	6	0.8	255	2	AD0940	triosephosphate is	790	6	0.8	273	2	F69199	conserved hypochet
718	6	0.8	255	2	AE0011	triose-phosphate i	791	6	0.8	273	2	S23281	homeotic protein m
719	6	0.8	255	2	D91234	triosephosphate is	792	6	0.8	274	2	A61030	nitrogenase (EC 1.
720	6	0.8	255	2	D86081	triosephosphate is	793	6	0.8	274	2	A43719	ured protein - Pro
721	6	0.8	255	2	AI1374	conserved hypochet	794	6	0.8	275	1	S78606	probable transport
722	6	0.8	255	2	AG1744	conserved hypochet	795	6	0.8	275	2	S27805	porin - slime mold
723	6	0.8	255	2	C90431	conserved hypochet	796	6	0.8	275	2	S66062	signal peptidase I
724	6	0.8	255	2	B87595	transcription regu	797	6	0.8	275	2	E83655	signal peptidase-1
725	6	0.8	256	2	C98869	trans-2-enoyl-ACP	798	6	0.8	275	2	S05299	hypothetical prote
726	6	0.8	256	2	A54322	corticotropin / li	799	6	0.8	276	1	S47640	adenyl-1-sulfate k
727	6	0.8	256	2	H69348	hypothetical prote	800	6	0.8	276	2	T29125	ketoacyl reductase
728	6	0.8	256	2	E95936	hypothetical prote	801	6	0.8	276	2	E83922	hypothetical prote
729	6	0.8	257	1	S22363	guFA protein homol	802	6	0.8	276	2	T48842	halorhodopsin [sai
730	6	0.8	257	2	H91119	guFA protein homol	803	6	0.8	276	2	C82136	septum site-determ
731	6	0.8	257	2	G85964	guFA protein homol	804	6	0.8	276	2	T38825	hypothetical prote
732	6	0.8	258	1	C69175	heat shock protein	805	6	0.8	277	1	H71220	hypothetical prote
733	6	0.8	258	2	C84758	hypothetical prote	806	6	0.8	277	1	S32571	malD protein - Str
734	6	0.8	258	2	T27393	hypothetical prote	807	6	0.8	277	2	H87213	conserved hypochet
735	6	0.8	259	2	H86809	oxidoreductase ypa	808	6	0.8	277	2	S03240	hypothetical prote
736	6	0.8	259	2	G98050	triose-phosphate i	809	6	0.8	277	2	E72564	hypothetical prote
737	6	0.8	259	2	J50660	homeotic protein H	810	6	0.8	277	2	G97783	hypothetical prote
738	6	0.8	259	2	A38284	homeotic protein Q	811	6	0.8	277	2	AD3386	phytoene synthase
739	6	0.8	260	2	S70599	cytochrome-c oxida	812	6	0.8	278	2	A84131	plant-metabolite d
740	6	0.8	260	2	AB2536	hypothetical prote	813	6	0.8	278	2	D64489	hypothetical prote
741	6	0.8	260	2	C95380	conserved hypochet	814	6	0.8	278	2	D75585	urease accessory p
742	6	0.8	261	2	S53423	major intrinsic pr	815	6	0.8	278	2	B70513	hypothetical prote
743	6	0.8	262	2	S72890	hypothetical prote	816	6	0.8	279	2	T09620	probable lectin 2
744	6	0.8	262	2	A70577	hypothetical prote	817	6	0.8	279	2	AH1182	transcription regu
745	6	0.8	263	2	T12407	NADH2 dehydrogenas	818	6	0.8	279	2	AH1882	nitrate transport
746	6	0.8	263	2	G64085	triose-phosphate i	819	6	0.8	279	2	G70807	hypothetical prote
747	6	0.8	263	2	A55279	major intrinsic pr	820	6	0.8	279	2	C75538	hypothetical prote
748	6	0.8	263	2	S73314	hypothetical prote	821	6	0.8	279	2	AI1012	hypothetical prote
749	6	0.8	263	2	I54780	APK1 antigen - hum	822	6	0.8	279	2	A83148	conserved hypochet
750	6	0.8	264	2	B71362	probable exodeoxyr	823	6	0.8	280	2	T07741	nitrate reductase
751	6	0.8	264	2	T10155	hypothetical prote	824	6	0.8	280	2	H95246	maltoextrin ABC t
752	6	0.8	264	2	AI2667	conserved hypochet	825	6	0.8	280	2	A82185	glycerol-3-phospha
753	6	0.8	265	2	D83287	hypothetical prote	826	6	0.8	280	2	T24454	hypothetical prote
754	6	0.8	265	2	A75448	rRNA methylase - D	827	6	0.8	281	1	MMECUE	sn-Glycerol-3-phos
755	6	0.8	265	2	S62363	D-2-chloropropioni	828	6	0.8	281	1	B64227	hypothetical prote
756	6	0.8	266	2	H70858	probable electron	829	6	0.8	281	1	S73813	lysophospholipase
757	6	0.8	266	2	S51833	acelin-4 precursor	830	6	0.8	281	2	AI1912	hypothetical prote
758	6	0.8	266	2	C96913	sulfate adenylate	831	6	0.8	281	2	A86012	hypothetical prote
759	6	0.8	266	2	PQ0393	genome polypeptide	832	6	0.8	281	2	A91166	hypothetical prote

833	6	0.8	281	2	C64241	hypothetical prote	906	0.8	296	2	F75209	hypothetical prote
834	6	0.8	281	2	T50208	yeast kt112 protei	907	0.8	297	2	G87187	phosphoribosylam
835	6	0.8	281	2	T01445	hypothetical prote	908	0.8	297	2	G70708	probable purC prot
836	6	0.8	281	2	F89045	protein B0238.3 [i	909	0.8	297	2	A72130	hypothetical prote
837	6	0.8	281	2	AF3407	transporter, dme f	910	0.8	297	2	H87613	pilus assembly pro
838	6	0.8	282	2	T06637	hypothetical prote	911	0.8	297	2	G95384	probable lytR-fami
839	6	0.8	282	2	A75473	probable sigma fac	912	0.8	297	2	AF2980	conserved hypothet
840	6	0.8	282	2	F82851	conserved hypothet	913	0.8	297	2	H98302	hypothetical prote
841	6	0.8	282	2	D97442	hypothetical prote	914	0.8	297	2	I54320	homeobox protein -
842	6	0.8	282	2	I41318	fimbrial adhesin K	915	0.8	297	2	A40560	homeotic protein H
843	6	0.8	283	1	T12062	xpek protein - xan	916	0.8	298	1	G69862	heat-shock protein
844	6	0.8	283	2	D83846	hypothetical prote	917	0.8	298	2	SI2635	apolipoprotein E p
845	6	0.8	284	2	B64694	conserved hypothet	918	0.8	298	2	D87450	transcription regu
846	6	0.8	284	2	H82119	probable transcrip	919	0.8	298	2	I40434	flagellar biosynth
847	6	0.8	284	2	A36604	hypothetical prote	920	0.8	298	2	T38937	rna-binding protei
848	6	0.8	284	2	T29001	hypothetical prote	921	0.8	298	2	T43542	RNA-binding protei
849	6	0.8	284	2	G71192	probable cobalt tr	922	0.8	298	2	T84224	hypothetical prote
850	6	0.8	284	2	A97492	probable transcrip	923	0.8	298	2	T33220	hypothetical prote
851	6	0.8	285	2	H71938	flagellar motor sw	924	0.8	299	2	PN0638	hypothetical prote
852	6	0.8	286	2	AF1298	hydrolase (importe	925	0.8	299	2	A99422	hypothetical prote
853	6	0.8	286	2	G69182	thiosulfate sulfur	926	0.8	299	2	B70737	permease (importe
854	6	0.8	286	2	H97341	dihydrodipicolinat	927	0.8	299	2	SI8813	hypothetical prote
855	6	0.8	286	2	A81969	probable chromosom	928	0.8	299	2	SI8813	hypothetical prote
856	6	0.8	287	1	S72569	probable aldehyde	929	0.8	300	2	AI3101	transcription regu
857	6	0.8	287	2	E98111	hypothetical prote	930	0.8	300	2	I40215	hypothetical prote
858	6	0.8	287	2	E82978	conserved hypothet	931	0.8	300	2	F75065	hypothetical prote
859	6	0.8	287	2	T24640	hypothetical prote	932	0.8	300	2	H75200	hypothetical prote
860	6	0.8	287	2	F64648	flly protein - Hel	933	0.8	300	2	D71234	hypothetical prote
861	6	0.8	287	2	AE3578	glycine betaine/l-	934	0.8	300	2	AF2846	permease (importe
862	6	0.8	288	2	AE3946	pyruvate synthase	935	0.8	300	2	F97623	hypothetical prote
863	6	0.8	288	2	C56281	7alpha-cephe-meth	936	0.8	301	2	C69837	5-oxo-1,2,5-tricar
864	6	0.8	288	2	SI8438	sporulation protei	937	0.8	301	2	C96961	probable membrane
865	6	0.8	288	2	A02091	probable exported	938	0.8	301	2	C96961	cell division prot
866	6	0.8	288	2	JS0659	homeotic protein H	939	0.8	302	1	WZBE9	gene 9 protein - h
867	6	0.8	289	1	S35294	probable glucose-1	940	0.8	302	2	T40490	probable 26S prote
868	6	0.8	289	1	S55649	deoxyuridine triph	941	0.8	302	2	F81016	conserved hypothet
869	6	0.8	289	2	A95158	homoserine kinase	942	0.8	302	2	F90158	DNA repair endo/ex
870	6	0.8	289	2	A98024	homoserine kinase	943	0.8	302	2	H82968	conserved hypothet
871	6	0.8	289	2	A02062	conserved hypothet	944	0.8	302	2	H87476	probable transcrip
872	6	0.8	289	2	H86522	CT144 hypothetical	945	0.8	302	2	B82968	probable transcrip
873	6	0.8	289	2	B72099	conserved hypothet	946	0.8	302	2	H87476	polyallic acid tr
874	6	0.8	289	2	C71501	probable outer mem	947	0.8	302	2	H87476	probable chemotaxi
875	6	0.8	289	2	B85794	hypothetical prote	948	0.8	302	2	S75481	ADP-ribosyl cyclas
876	6	0.8	289	2	S75197	ABC-type transport	949	0.8	302	2	AC0092	hypothetical prote
877	6	0.8	290	1	KIRFAS	phosphoribulokinas	950	0.8	302	2	F71680	hypothetical prote
878	6	0.8	290	2	A86038	involved in lipopo	951	0.8	302	2	S75557	conserved hypothet
879	6	0.8	290	2	H91190	hypothetical prote	952	0.8	302	2	H81818	hypothetical prote
880	6	0.8	290	2	S47839	short-chain dehydr	953	0.8	302	2	B47089	probable AraC-type
881	6	0.8	291	2	AH3074	probable short-cha	954	0.8	302	2	B96909	probable permease
882	6	0.8	291	2	A96212	conserved hypothet	955	0.8	302	2	G71166	hypothetical prote
883	6	0.8	291	2	A81659	phosphoribulokinas	956	0.8	302	2	B69449	conserved hypothet
884	6	0.8	292	1	B35819	probable membrane	957	0.8	302	2	T46647	pyridoxine biosynt
885	6	0.8	292	2	D97199	hypothetical prote	958	0.8	302	2	T03155	ribonucleoside-dip
886	6	0.8	292	2	S23239	4-hydroxybenzoate	959	0.8	302	2	T03155	acyltransferase (E
887	6	0.8	293	1	D69300	hypothetical prote	960	0.8	302	2	UN0518	mrr restriction sy
888	6	0.8	293	2	A89818	conserved hypothet	961	0.8	302	2	AD2494	hypothetical prote
889	6	0.8	293	2	AH1095	rRNA methyltransfe	962	0.8	302	2	E64138	phosphoribosylam
890	6	0.8	293	2	JN0651	conserved hypothet	963	0.8	302	2	A89952	primosomal protein
891	6	0.8	293	2	B75441	hypothetical prote	964	0.8	302	2	E64138	inosine-uridine pr
892	6	0.8	293	2	T32229	transcription regu	965	0.8	302	2	AF3230	inosine-uridine pr
893	6	0.8	293	2	A97313	probable membrane	966	0.8	302	2	T36764	transcriptional re
894	6	0.8	293	2	AH0143	tissue factor prec	967	0.8	302	2	H83660	probable ABC-type
895	6	0.8	294	1	KFWS3	NADH2 dehydrogenas	968	0.8	302	2	AI1269	cysteine synthase
896	6	0.8	294	2	T11379	probable endonucle	969	0.8	302	2	AB1632	primosome componen
897	6	0.8	294	2	T35492	H+-transporting tw	970	0.8	302	2	G90270	hypothetical prote
898	6	0.8	294	2	B81427	hypothetical prote	971	0.8	302	2	G69211	Na+/Ca2+ exchangin
899	6	0.8	294	2	G97449	conserved hypothet	972	0.8	302	2	T24423	conserved hypothet
900	6	0.8	295	2	F69976	30S ribosomal prot	973	0.8	302	2	S70735	hypothetical prote
901	6	0.8	295	2	A60131	homeotic protein X	974	0.8	302	2	D69348	conserved hypothet
902	6	0.8	295	2	D75597	glucose-1-phosphat	975	0.8	302	2	A99993	hypothetical prote
903	6	0.8	296	2	E71717	ribosomal protein	976	0.8	302	2	D97607	tropinesterase (at
904	6	0.8	296	2	S39746	hypothetical prote	977	0.8	302	2	D64752	dihydrodipicolinat
905	6	0.8	296	2			978	0.8	302	2	C83136	probable epimerase

979	6	0.8	309	2	F97168	nucleoside-diphosp
980	6	0.8	309	2	G85988	probable transcrip
981	6	0.8	309	2	E65116	hypothetical prote
982	6	0.8	309	2	D91143	probable transcrip
983	6	0.8	309	2	T20518	hypothetical prote
984	6	0.8	309	2	T38671	Zinc finger, C3HC4
985	6	0.8	310	2	C47045	ferrochelatase (EC
986	6	0.8	310	2	A12654	glycyl-tRNA synthe
987	6	0.8	310	2	S45130	autophagocytosis p
988	6	0.8	310	2	H82439	hypothetical prote
989	6	0.8	310	2	AG1733	gp49 (Bacteriophag
990	6	0.8	310	2	B75476	conserved hypotet
991	6	0.8	310	2	G84809	hypothetical prote
992	6	0.8	311	2	I64082	pantothenate kinas
993	6	0.8	311	2	T11532	phosphoribosylamin
994	6	0.8	311	2	G75121	nucleolar protein
995	6	0.8	311	2	F95349	hypothetical prote
996	6	0.8	311	2	H75411	conserved hypotet
997	6	0.8	311	2	A83329	probable phosphati
998	6	0.8	311	2	E70599	hypothetical prote
999	6	0.8	312	1	S46047	probable 3-methyl-
1000	6	0.8	312	2	T08076	adenyl-yl-sulfate k
ALIGNMENTS						
RESULT 1						
outer membrane protein OMP85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491 s						
C;Species: Neisseria meningitidis						
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004						
C;Accession: D82000						
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel						
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,						
Nature 404, 502-506, 2000						
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.						
A;Reference number: AB1775; MUID:20222556; PMID:10761919						
A;Accession: D82000						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-797 <PAR>						
A;Cross-references: UNIPROT:Q9JX31; UNIPARC:UPI0000003C425; GB:AL162752; GB:AL157959; NID						
A;Experimental source: serogroup A, strain Z2491						
C;Genetics:						
A;Gene: Omp85; NMA0085						
C;Superfamily: protective surface antigen D-15						
Query Match 94.4%; Score 752; DB 2; Length 797;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	21	ADFTIQDIRVEGLQRTPESTVFNFLPVKVGDTYNDTHGSAIKSLYATGFFDDVRVETAD 80				
Db	21	ADFTIQDIRVEGLQRTPESTVFNFLPVKVGDTYNDTHGSAIKSLYATGFFDDVRVETAD 80				
Qy	81	GQLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSQYFNQATLNQAVAGLKEEY 140				
Db	81	GQLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSQYFNQATLNQAVAGLKEEY 140				
Qy	141	LGRGKLNITQTPKVKTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQMSLITE 200				
Db	141	LGRGKLNITQTPKVKTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQMSLITE 200				
Qy	201	GGIWTWLTNRNQNEOKFAQDMKVTFYQNNGYFDFRILDTDTQTNEDTKTKQIKITVH 260				
Db	201	GGIWTWLTNRNQNEOKFAQDMKVTFYQNNGYFDFRILDTDTQTNEDTKTKQIKITVH 260				
Qy	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKGYERQQTAVLGEIQNRMGSGAGYAS 320				
Db	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKGYERQQTAVLGEIQNRMGSGAGYAS 320				
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYNEIHITGNKTRDEVVRELQMESAPYDTS 380				

Db	321	EISVQPLPNAETKTVDVFLHIEPGRKIYNEIHITGNKTRDEVVRELQMESAPYDTS 380				
Qy	381	KLQRSKERVELLGYFQNVQFDVAVPLAGTDPKVDLNNMSLTERSTGSLDLGAGWQDTGLVM 440				
Db	381	KLQRSKERVELLGYFQNVQFDVAVPLAGTDPKVDLNNMSLTERSTGSLDLGAGWQDTGLVM 440				
Qy	441	SAGVSQDNILFGTCKSAALRASRSKTTLNGSLSTDDYFTADGYSLGVDVYVYKAPDRKAS 500				
Db	441	SAGVSQDNILFGTCKSAALRASRSKTTLNGSLSTDDYFTADGYSLGVDVYVYKAPDRKAS 500				
Qy	501	TSIKQVKTITAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560				
Db	501	TSIKQVKTITAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560				
Qy	561	TDGSFQWLYKGTVGWGRNKTDLSALWPTRGYLTGVNAEIALPGSLQYVSATHNQWTFPP 620				
Db	561	TDGSFQWLYKGTVGWGRNKTDLSALWPTRGYLTGVNAEIALPGSLQYVSATHNQWTFPP 620				
Qy	621	LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSGVRYESGTLGPKVYDEYGEKIS 680				
Db	621	LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSGVRYESGTLGPKVYDEYGEKIS 680				
Qy	681	YGGNKKANYSAEILFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740				
Db	681	YGGNKKANYSAEILFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740				
Qy	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772				
Db	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772				
RESULT 2						
G81228						
outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58 s						
C;Species: Neisseria meningitidis						
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004						
C;Accession: G81228						
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.						
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;						
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.						
Science 287, 1809-1815, 2000						
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver						
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.						
A;Reference number: AB1000; MUID:20175755; PMID:10710307						
A;Accession: G81228						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-797 <TET>						
A;Cross-references: UNIPROT:Q9K1H0; UNIPARC:UPI0000003C41F; GB:AE002375; GB:AE002098; NID						
A;Experimental source: serogroup B, strain MC58						
C;Genetics:						
A;Gene: NMB0182						
C;Superfamily: protective surface antigen D-15						
Query Match 94.4%; Score 752; DB 2; Length 797;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	21	ADFTIQDIRVEGLQRTPESTVFNFLPVKVGDTYNDTHGSAIKSLYATGFFDDVRVETAD 80				
Db	21	ADFTIQDIRVEGLQRTPESTVFNFLPVKVGDTYNDTHGSAIKSLYATGFFDDVRVETAD 80				
Qy	81	GQLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSQYFNQATLNQAVAGLKEEY 140				
Db	81	GQLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSQYFNQATLNQAVAGLKEEY 140				
Qy	141	LGRGKLNITQTPKVKTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQMSLITE 200				
Db	141	LGRGKLNITQTPKVKTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQMSLITE 200				
Qy	201	GGIWTWLTNRNQNEOKFAQDMKVTFYQNNGYFDFRILDTDTQTNEDTKTKQIKITVH 260				
Db	201	GGIWTWLTNRNQNEOKFAQDMKVTFYQNNGYFDFRILDTDTQTNEDTKTKQIKITVH 260				
Qy	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKGYERQQTAVLGEIQNRMGSGAGYAS 320				
Db	261	EGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKGYERQQTAVLGEIQNRMGSGAGYAS 320				
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYNEIHITGNKTRDEVVRELQMESAPYDTS 380				

Db 201 GGIWTLTRSNQFNEQFAQDMKVTDFYQNNGYDFRILDTDIQTNEKDTKQTIKIVH 260
Qy 261 EGGRFRWGVKSI EGDNTNEVPKAELEKLTMRKPKWYERQOMTAVLGEIQNRMGSGAGVAYS 320
Db 261 EGGRFRWGVKSI EGDNTNEVPKAELEKLTMRKPKWYERQOMTAVLGEIQNRMGSGAGVAYS 320
Qy 321 EISVQPLNAETKTVDVFLHIETPGRKIVYVNEIHTGNKNTDEVRRELROMESAPYDTS 380
Db 321 EISVQPLNAETKTVDVFLHIETPGRKIVYVNEIHTGNKNTDEVRRELROMESAPYDTS 380
Qy 381 KLORSKERVVELLYGFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLORSKERVVELLYGFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFGTGKSAALRASRKTTLNGSLSFDTDPYTAGVSLGVYVYKAFDPRKAS 500
Db 441 SAGVSQDNLFGTGKSAALRASRKTTLNGSLSFDTDPYTAGVSLGVYVYKAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIIKYGKTDG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIIKYGKTDG 560
Qy 561 TDGSPFKMLYKGTGCGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNOTWFFP 620
Db 561 TDGSPFKMLYKGTGCGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNOTWFFP 620
Qy 621 LSKTFTMLGSGVGIAGGYGRKTEIPFPENFYGGGLGSRVGSCTLGPVKYVDEYGEKIS 680
Db 621 LSKTFTMLGSGVGIAGGYGRKTEIPFPENFYGGGLGSRVGSCTLGPVKYVDEYGEKIS 680
Qy 681 YGCKKANKVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYG 740
Db 681 YGCKKANKVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSSAGGAVTWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSSAGGAVTWLSPLGPMKF 772

RESULT 3
T46206
hypothetical protein T8P19.130 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46206
R:Choisne, N.; Robert, C.; Bröttier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223008
A:Accession: T46206
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <CHO>
A:Cross-references: UNIPROT:Q9SMN7; UNIPARC:UPI000000A5A5F; EMBL:AL133315
A:Experimental source: cultivar Columbia; BAC clone T8P19
C:Genetics:
A:Map position: 3
A:Introns: 39/2; 62/3; 94/3; 133/2; 179/3; 277/1
A:Note: T8P19.130

Query Match 1.1%; Score 9; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSVRGY 662
Db 152 GGLGSVRGY 160

RESULT 4
T49132
hypothetical protein F26G5.110 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T49132
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A:Reference number: 225017
A:Accession: T49132
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <DAN>
A:Cross-references: UNIPROT:Q9LXP7; UNIPARC:UPI000000A38BD; EMBL:AL353814; GSPDB:GN000661;
A:Experimental source: cultivar Columbia; BAC clone F26G5
C:Genetics:
A:Map position: 3
A:Introns: 12/1; 34/2; 135/3; 188/3; 212/2; 238/3; 277/2; 326/3; 350/1; 395/1

Query Match 1.1%; Score 9; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSVRGY 662
Db 296 GGLGSVRGY 304

RESULT 5
A96984
hypothetical protein CAC0683 [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: A96984
R:Nolling, J.; Breston, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4836, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A96984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <KUR>
A:Cross-references: UNIPROT:Q97L79; UNIPARC:UPI000000C9F47; GB:AE001437; PIDN:AAK78660.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0683

Query Match 1.0%; Score 8; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 670 KVDYDEYGE 677
Db 17 KVDYDEYGE 24

RESULT 6
E84423
hypothetical protein At2G01340 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: E84423
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, J.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84423
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <STO>
A:Cross-references: UNIPROT:Q9ZU33; UNIPARC:UPI000000A4EBB; GB:AE002093; NID:G4262241;
C:Genetics:
A:Gene: At2G01340
A:Map position: 2

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Query Match      1.0%; Score 8; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      280 PKAELEKL 287
      |||||
Db      144 PKAELEKL 151

RESULT 7
glycerate dehydrogenase PAB2374 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C:Accession: B75057
R:anonymous, Genoscope
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: B75057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <KAW>
A:Cross-references: UNIPROT:Q9UVRL1; UNIPARC:UPI0000034704; GB:AJ248287; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: gdh-like; PAB2374
C:Superfamily: Phosphoglycerate dehydrogenase

Query Match      1.0%; Score 8; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      485 LGYDVYVK 492
      |||||
Db      145 LGYDVYVK 152

RESULT 8
formate dehydrogenase accessory protein VC1519 [imported] - Vibrio cholerae (strain N169)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: C82190
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833; PMID:10952301
A:Accession: C82190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <HEI>
A:Cross-references: UNIPROT:Q9KRW5; UNIPARC:UPI00000C2FF4; GB:AE004230; GB:AE003852; NID
A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor
C:Genetics:
A:Gene: VC1519
A:Map position: 1
C:Superfamily: formate dehydrogenase accessory protein FdhD

Query Match      1.0%; Score 8; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      671 VYDEYGEK 678
      |||||
Db      81 VYDEYGEK 88

RESULT 9
A:Title:
A:Reference number:
A:Accession:
A:Molecule type: DNA
A:Residues:

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probable dehydrogenase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 31-Dec-2004
C:Accession: A71175
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamanoto, S.; Sekine,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: A71175
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <KAW>
A:Cross-references: UNIPROT:O58320; UNIPARC:UPI00000667F3; GB:AF000002; NID:G3236129; PFI
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0597
C:Superfamily: D-3-phosphoglycerate dehydrogenase with ACT domain

Query Match      1.0%; Score 8; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      485 LGYDVYVK 492
      |||||
Db      186 LGYDVYVK 193

RESULT 10
T04985
Probable transaminase (EC 2.6.1.-) T16L1.170 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04985
R;Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15393
A:Accession: T04985
A:Molecule type: DNA
A:Residues: 1-426 <BEV>
A:Cross-references: UNIPROT:O81885; UNIPARC:UPI0000048A52; EMBL:AL031394
A:Experimental source: cultivar Columbia; BAC clone T16L1
C:Genetics:
A:Map position: 4
A:Introns: 19/1; 41/3; 80/3; 101/3; 136/3; 153/3; 260/3; 329/3
A:Note: T16L1.170
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match      1.0%; Score 8; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      484 SLGYDVYVG 491
      |||||
Db      351 SLGYDVYVG 358

RESULT 11
G42365
flagellar hook-length control protein fliK - Bacillus subtilis
N:Alternate names: hypothetical protein 7 (flaA operon)
C:Species: Bacillus subtilis
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C:Accession: G42365; G69624; S14500
R;Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A:Title: The flaA locus of Bacillus subtilis is part of a large operon coding for flagell
A:Reference number: A42365; MUID:91258343; PMID:1828465
A:Accession: G42365
A:Molecule type: DNA
A:Residues: 1-429 <ALB>

```

A:Cross-references: UNIPROT:P23451; UNIPARC:UPI00000603E2; EMBL:X56049; NID:G39904; PIDN:R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho, A.; Ehrlich, S.D.; Emmeron, P.F.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.; Koester, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A:Authors: Schlegel, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrala, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*. A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: G69624

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-429 <KUN>

A:Cross-references: UNIPARC:UPI00000603E2; GB:Z99112; GB:AL009126; NID:G2633902; PIDN:CA

A:Experimental source: strain 168

C:Genetics:

A:Gene: flik

Query Match 1.0%; Score 8; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 328 PNAETKTV 335
|||||||

Db 286 PNAETKTV 293

RESULT 12

IMBP4

site-specific recombinase for integration and excision - *Bacillus phage phi-105*

N:Alternate names: immunity region protein 3, 4, 5, 6

C:Species: *Bacillus phage phi-105*

C>Date: 31-Dec-1988 #sequence revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T13541; D24521; D24521; F24521

R:Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y. submitted to the EMBL Data Library, July 1998

A:Description: Complete nucleotide sequence of *Bacillus subtilis* phage phi-105.

A:Reference number: Z17688

A:Accession: T13541

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-474 <KOB>

A:Cross-references: UNIPROT:Q9T200; UNIPARC:UPI000009B54B; EMBL:AB016282; PIDN:BAA36658.

R:Cully, D.F.; Garro, A.J.

Gene 38, 153-164, 1985

A:Title: Nucleotide sequence of the immunity region of *Bacillus subtilis* bacteriophage phi-105.

A:Reference number: A91535; MUID:86056972; PMID:3934047

A:Accession: C24521

A:Molecule type: DNA

A:Residues: 1-78, 'MTHC' <CUL>

A:Cross-references: UNIPARC:UPI000013B43C; GB:M11920; NID:G215477; PIDN:AAA88399.1; PID:

A:Accession: D24521

A:Molecule type: DNA

A:Residues: 149-160, 'AR', '163', 'H', 'HSDSQRRVR', '381-383', 'RIQRARS', '392 <CU2>

A:Cross-references: UNIPARC:UPI000013B43D; GB:M11920; NID:G215477; PIDN:AAA88401.1; PID:

A:Accession: E24521

A:Molecule type: DNA

A:Residues: 189-318, 'HAP', <CU3>

A:Cross-references: UNIPARC:UPI0000174BB8; GB:M11920

A:Accession: F24521

A:Molecule type: DNA

A:Residues: 'MP', '319-376', 'RNTK', '381', 'PGPWS' <CU4>

A:Cross-references: UNIPARC:UPI0000174BB9; GB:M11920

C:Superfamily: phage phi-105 site-specific recombinase

C:Keywords: early protein

Query Match 1.0%; Score 8; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 IDEGKSAK 175
|||||||

Db 53 IDEGKSAK 60

RESULT 13

GB83375

probable glycosyl hydrolase PA2164 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C:Species: *Pseudomonas aeruginosa*

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C:Accession: G83375

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.B.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G83375

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-583 <STO>

A:Cross-references: UNIPROT:Q9I1V1; UNIPARC:UPI000000C55E1; GB:AE004643; GB:AE004091; NID

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA2164

C:Superfamily: glycosyltrehalose trehalohydrolase

Query Match 1.0%; Score 8; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 74 VRVETADG 81
|||||||

Db 29 VRVETADG 36

RESULT 14

JE0327

dynamin-related protein MSPI - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: JE0327

R:Pellicoquin, L.; Belenguer, P.; Menon, Y.; Ducommun, B. Biochem. Biophys. Res. Commun. 251, 720-726, 1998

A:Title: Identification of a fission yeast dynamin-related protein involved in mitochond

A:Reference number: JE0327; MUID:99008891; PMID:9790976

A:Accession: JE0327

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-903 <PEL>

A:Cross-references: UNIPROT:P87320; UNIPARC:UPI0000169165; GB:Y07891; NID:G2231081; PIDN:

C:Genetics:

A:Gene: MSPI

Query Match 1.0%; Score 8; DB 2; Length 903;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 455 SAALRASR 462
|||||||

Db 417 SAALRASR 424

RESULT 15

TS0334

dynamin-related protein [imported] - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C;Accession: T50334
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25062
A;Accession: T50334
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-903 <LYN>
A;Cross-references: UNIPROT:P87320; UNIPARC:UPI000012F637; EMBL:AL157874; PIDN:CAB75996
A;Experimental source: strain 972h(-); cosmid c1718
C;Genetics:
A;Gene: SPDB:SPBC1718.06
A;Map position: 2

Query Match 1.0%; Score 8; DB 2; Length 903;
Best Local Similarity 100.0%; Pred.No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 455 SAALRASR 462
Db 417 SAALRASR 424

Search completed: April 12, 2006, 16:23:44
Job time : 67 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 12, 2006, 16:14:58 ; Search time 190 Seconds
(without alignments)
1843.078 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MLLKQIASALMLGISPLAF.....LKKPEDEIQRFQQLGTTF 797

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2441997

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	3	AAY84947 Amino aci
2	797	100.0	797	5	ABD79802 Neisseria
3	797	100.0	797	9	AD209417 Neisseria
4	752	94.4	797	4	AU03959 Neisseria
5	752	94.4	797	4	AU03957 Neisseria
6	752	94.4	797	4	AU04451 Neisseria
7	752	94.4	797	4	AU04451 Neisseria
8	752	94.4	797	4	AU04451 Neisseria
9	752	94.4	797	4	AU04451 Neisseria
10	752	94.4	797	4	AU04451 Neisseria
11	752	94.4	797	4	AU04451 Neisseria
12	210	26.3	792	4	AU03958 Neisseria
13	210	26.3	792	4	AU03958 Neisseria
14	210	26.3	792	4	AU03958 Neisseria
15	210	26.3	792	6	ABP80499 N. gonorr
16	210	26.3	792	6	ABP79748 N. gonorr
17	157	19.7	792	3	ABP84946 Amino aci
18	157	19.7	792	5	ABG91064 Neisseria
19	157	19.7	792	5	ABD79801 Neisseria
20	157	19.7	792	9	AD209415 Neisseria
21	37	4.6	37	4	AU03997 Neisseria
22	32	4.0	32	4	AU04410 Neisseria
23	29	3.6	29	4	AU03987 Neisseria
24	25	3.1	25	4	AU04412 Neisseria

98	8	1.0	116	3	AAG57649	Aag57649	Arabidops	171	7	0.9	83	4	AAU60561	Aau60561	Propionib
99	8	1.0	117	3	AAG49893	Aag49893	Arabidops	172	7	0.9	83	6	ABM57080	Abm57080	Propionib
100	8	1.0	126	3	AAG25176	Aag25176	Arabidops	173	7	0.9	85	8	ADS42710	Adas42710	Bacterial
101	8	1.0	201	3	AAG57648	Aag57648	Arabidops	174	7	0.9	86	6	ADA34965	Ada34965	Aginetoba
102	8	1.0	202	3	AAG49892	Aag49892	Arabidops	175	7	0.9	86	7	ABO63968	Abog63968	Klebsiell
103	8	1.0	214	3	AAG57647	Aag57647	Arabidops	176	7	0.9	87	4	AAU17729	Aau17729	Novel hum
104	8	1.0	215	3	AAG49891	Aag49891	Arabidops	177	7	0.9	87	7	ADG41109	Adg41109	Human res
105	8	1.0	216	5	ADN21670	Adn21670	Bacterial	178	7	0.9	87	7	AD196883	Adi96883	Human res
106	8	1.0	217	5	ABG60322	Abg60322	Yeast dyn	179	7	0.9	88	3	AAV86404	Aay86404	Human gen
107	8	1.0	250	8	ADX88498	Adx88498	Plant ful	180	7	0.9	88	6	ABO53551	Abos3551	Novel hum
108	8	1.0	266	4	ABG15869	Abg15869	Novel hum	181	7	0.9	92	7	ADE08224	Ade08224	Novel pro
109	8	1.0	266	7	ADC32990	Adc32990	Human nov	182	7	0.9	96	4	AAU64929	Aau64929	Propionib
110	8	1.0	274	9	ABM96353	Abm96353	M. xanthu	183	7	0.9	96	6	ABM61448	Abm61448	Propionib
111	8	1.0	289	3	AAG49003	Aag49003	Arabidops	184	7	0.9	97	7	ABO69614	Abog69614	Pseudomon
112	8	1.0	299	4	AAG90486	Aag90486	C glutami	185	7	0.9	101	4	ABB17344	Abb17344	Human ner
113	8	1.0	315	8	ADS24860	Ads24860	Bacterial	186	7	0.9	102	7	ADM27054	Adm27054	Hyperther
114	8	1.0	321	8	ADU02334	Adu02334	Novel hum	187	7	0.9	110	3	AAG02520	Aag02520	Human sec
115	8	1.0	335	4	ABN96813	Abn96813	Putative	188	7	0.9	110	4	AAO06467	Aao06467	Human pol
116	8	1.0	336	8	ADN47487	Adn47487	Thermococ	189	7	0.9	119	5	ABP07824	Abp07824	Human ORF
117	8	1.0	349	3	AAG49002	Aag49002	Arabidops	190	7	0.9	120	4	AAU40749	Aau40749	Propionib
118	8	1.0	349	3	AAG49898	Aag49898	Arabidops	191	7	0.9	120	6	ABM37268	Abm37268	Propionib
119	8	1.0	397	3	AAG49898	Aag49898	Arabidops	192	7	0.9	121	3	AAG14889	Aag14889	Arabidops
120	8	1.0	409	3	AAG49001	Aag49001	Arabidops	193	7	0.9	122	4	AAM86629	Aam86629	Human imm
121	8	1.0	422	8	ADS23854	Ads23854	Bacterial	194	7	0.9	122	8	ADT57959	Adt57959	Plant pol
122	8	1.0	426	3	AAG49897	Aag49897	Arabidops	195	7	0.9	125	6	ABM69954	Abm69954	Phototrab
123	8	1.0	426	5	ABB93220	Abb93220	Herbicida	196	7	0.9	126	4	ABM69082	Abm69082	Drosophil
124	8	1.0	428	3	AAG14941	Aag14941	Arabidops	197	7	0.9	129	7	ADP04752	Adp04752	Bacterial
125	8	1.0	438	3	AAG14940	Aag14940	Arabidops	198	7	0.9	132	4	ABB11237	Abb11237	Human pho
126	8	1.0	445	4	ABG17863	Abg17863	Novel hum	199	7	0.9	143	3	AAG14888	Aag14888	Arabidops
127	8	1.0	451	3	AAG06359	Aag06359	Arabidops	200	7	0.9	150	6	ABU26587	Abu26587	Protein e
128	8	1.0	454	3	AAG14939	Aag14939	Arabidops	201	7	0.9	157	7	ADF07373	Adf07373	Bacterial
129	8	1.0	461	3	AAG06358	Aag06358	Arabidops	202	7	0.9	170	3	AAG21405	Aag21405	Arabidops
130	8	1.0	479	3	AAG06357	Aag06357	Arabidops	203	7	0.9	171	6	ABU01664	Abu01664	S. pneumo
131	8	1.0	494	8	ADS24095	Ads24095	Bacterial	204	7	0.9	176	8	ADX79668	Adx79668	Plant ful
132	8	1.0	583	8	ADS14924	Ads14924	Pseudomon	205	7	0.9	176	9	ABM97170	Abm97170	M. xanthu
133	8	1.0	648	7	ABO75882	AbO75882	Pseudomon	206	7	0.9	178	2	AAV45288	Aay45288	Human sec
134	8	1.0	745	4	ABG03852	Abg03852	Novel hum	207	7	0.9	178	2	AAV30708	Aay30708	Amino aci
135	8	1.0	745	4	ABG09109	Abg09109	Novel hum	208	7	0.9	179	7	ABO75778	AbO75778	Pseudomon
136	8	1.0	745	4	ABG10367	Abg10367	Novel hum	209	7	0.9	181	9	ADM17088	Adm17088	Eucalyptu
137	8	1.0	745	4	ABG14890	Abg14890	Novel hum	210	7	0.9	182	3	AAG22490	Aag22490	Arabidops
138	8	1.0	897	8	ADP98989	Adp98989	C. albica	211	7	0.9	186	8	ADT58920	Adt58920	Plant pol
139	8	1.0	1577	6	ABU41145	Abu41145	Protein e	212	7	0.9	189	4	ABG23074	Abg23074	Novel hum
140	8	1.0	1589	7	ADF04713	Adf04713	Bacterial	213	7	0.9	190	8	ADU02422	Adu02422	Novel hum
141	7	0.9	7	4	AAU04432	Aau04432	Neisseria	214	7	0.9	193	7	ABO59082	AbO59082	Pseudomon
142	7	0.9	7	4	AAU04441	Aau04441	Neisseria	215	7	0.9	194	4	ADM20062	Adm20062	Protein e
143	7	0.9	7	4	AAU04446	Aau04446	Neisseria	216	7	0.9	195	5	ABU52193	Abu52193	Helicobac
144	7	0.9	7	4	AAU03969	Aau03969	Neisseria	217	7	0.9	195	8	ADP30464	Adp30464	Human sec
145	7	0.9	7	4	AAU04437	Aau04437	Neisseria	218	7	0.9	196	3	AAG22489	Aag22489	Arabidops
146	7	0.9	7	4	AAU04419	Aau04419	Neisseria	219	7	0.9	197	8	ADX73180	Adx73180	Plant ful
147	7	0.9	7	4	AAU04429	Aau04429	Neisseria	220	7	0.9	199	8	ADU17845	Adu17845	Reverse t
148	7	0.9	7	4	AAU04443	Aau04443	Neisseria	221	7	0.9	200	8	ADP30686	Adp30686	Human sec
149	7	0.9	7	4	AAU04433	Aau04433	Neisseria	222	7	0.9	208	4	ABM68565	Abm68565	Drosophil
150	7	0.9	23	3	AAV65830	Aav65830	Mismatch	223	7	0.9	213	7	ABO68534	AbO68534	Pseudomon
151	7	0.9	27	9	ADV53219	Adv53219	Hedgehog	224	7	0.9	213	8	ABO60429	AbO60429	Human gen
152	7	0.9	35	9	ADY97222	Ady97222	Herpes si	225	7	0.9	217	8	ADX68977	Adx68977	Plant ful
153	7	0.9	50	4	AAAM20158	Aam20158	Peptide #	226	7	0.9	219	8	ADZ64459	Adz64459	Human can
154	7	0.9	50	4	ABB40395	Abb40395	Peptide #	227	7	0.9	221	8	ADN25744	Adn25744	Bacterial
155	7	0.9	50	4	AAAM34101	Aam34101	Peptide #	228	7	0.9	226	4	ABB67771	Abb67771	Drosophil
156	7	0.9	50	4	ABB24767	Abb24767	Protein #	229	7	0.9	226	6	ABM68435	Abm68435	Phototrab
157	7	0.9	50	4	AAAM73922	Aam73922	Human bon	230	7	0.9	228	8	ADSA2499	Adsa2499	Bacterial
158	7	0.9	50	4	AAAM61203	Aam61203	Human bra	231	7	0.9	232	4	AAUS9216	Aaus9216	Propionib
159	7	0.9	50	4	ABG55674	Abg55674	Human liv	232	7	0.9	232	6	ABM55735	Abm55735	Propionib
160	7	0.9	50	5	ABG43810	Abg43810	Human pep	233	7	0.9	233	5	ABU51725	Abu51725	Helicobac
161	7	0.9	56	8	ADN46996	Adn46996	Thermococ	234	7	0.9	234	2	AAW98579	Aaw98579	H. pylori
162	7	0.9	58	2	AAW48931	Aaw48931	Schwannom	235	7	0.9	243	4	ABG24253	Abg24253	Novel hum
163	7	0.9	60	3	AAAG03150	Aag03150	Human sec	236	7	0.9	244	6	ABM70306	Abm70306	Phototrab
164	7	0.9	61	4	AAU65753	Aau65753	Propionib	237	7	0.9	244	7	ABO67562	AbO67562	Klebsiell
165	7	0.9	61	6	ABM62272	Abm62272	Propionib	238	7	0.9	250	4	ABBS9528	Abbs9528	Drosophil
166	7	0.9	69	4	AAAM88690	Aam88690	Human imm	239	7	0.9	253	8	ADL04906	Adl04906	M. catarr
167	7	0.9	75	7	ADCO0302	Adc00302	Enterohae	240	7	0.9	255	8	ADM92238	Adm92238	S. pneumo
168	7	0.9	76	6	ABU15436	Abu15436	Protein e	241	7	0.9	255	8	ADM92238	Adm92238	S. pneumo
169	7	0.9	78	4	AAAM90288	Aam90288	Human imm	242	7	0.9	257	7	ABO82478	AbO82478	Pseudomon
170	7	0.9	82	5	ABP33075	Abp33075	Human ORF	243	7	0.9	260	9	ABM96630	Abm96630	M. xanthu

244	7	0.9	263	7	ABO77554	Pseudomon	317	7	0.9	357	7	ABO84393	Pseudomon
245	7	0.9	265	3	AA95697	Comid cH	318	7	0.9	357	6	ABM93822	M. xanthu
246	7	0.9	268	7	ABO74392	Pseudomon	319	7	0.9	359	6	AAE36463	Human col
247	7	0.9	268	7	ABO83252	Pseudomon	320	7	0.9	359	8	ADP55871	Human PRO
248	7	0.9	268	7	ABO74393	Pseudomon	321	7	0.9	363	9	ADV67077	A. fumiga
249	7	0.9	270	7	ABO74440	Pseudomon	322	7	0.9	363	9	ABM96815	M. xanthu
250	7	0.9	277	2	AA937752	Amino aci	323	7	0.9	366	2	AAW69392	Aspergill
251	7	0.9	277	8	ADQ81750	Trypanoso	324	7	0.9	366	8	ADN18365	Bacterial
252	7	0.9	280	5	ADP26998	Streptoco	325	7	0.9	367	7	ADI60171	Secreted
253	7	0.9	280	6	ABU46897	Protein e	326	7	0.9	379	7	ABM87030	Rice abio
254	7	0.9	282	6	ADA54528	Human pro	327	7	0.9	382	2	AA45261	Human sec
255	7	0.9	282	7	ADC95911	E. faeciu	328	7	0.9	383	4	AA991116	C glucami
256	7	0.9	285	6	ABU45032	Protein e	329	7	0.9	386	4	ABG21113	Novel hum
257	7	0.9	288	6	ABR53144	Protein s	330	7	0.9	386	8	ADN26073	Bacterial
258	7	0.9	288	7	ADK63118	Disease t	331	7	0.9	387	8	ADP31368	Human sec
259	7	0.9	288	8	ADS44003	Bacterial	332	7	0.9	387	9	ABU21102	Novel hum
260	7	0.9	288	4	ABB10987	Human WD-	333	7	0.9	390	6	ABU20261	Protein e
261	7	0.9	290	4	AAW79660	Human pro	334	7	0.9	392	8	ADP29346	Human sec
262	7	0.9	290	4	AAW79660	Human pro	335	7	0.9	392	8	ABO68025	Pseudomon
263	7	0.9	291	7	ABO79608	Pseudomon	336	7	0.9	393	7	AAW29659	Homo eapi
264	7	0.9	292	7	ABO79608	Pseudomon	337	7	0.9	397	2	AAW29659	Homo eapi
265	7	0.9	292	6	ABU29077	Protein e	338	7	0.9	397	2	AAW29659	Homo eapi
266	7	0.9	293	8	ADS24291	Bacterial	339	7	0.9	399	4	AAU32410	Novel hum
267	7	0.9	294	7	ADC94620	E. faeciu	340	7	0.9	399	8	ADP31313	Human sec
268	7	0.9	300	7	ABO63156	Klebsiell	341	7	0.9	405	4	AAW93419	Human pro
269	7	0.9	305	8	ADN17987	Bacterial	342	7	0.9	405	8	ADN25996	Bacterial
270	7	0.9	307	3	AG22488	Arabidops	343	7	0.9	405	8	ADS42259	Bacterial
271	7	0.9	310	8	ADS23653	Bacterial	344	7	0.9	406	4	AAW39653	Human pol
272	7	0.9	310	9	AEA20290	Novel hum	345	7	0.9	406	6	ABU96684	Human nuc
273	7	0.9	314	3	AG21404	Arabidops	346	7	0.9	410	5	ABP29775	Streptoco
274	7	0.9	315	4	AAW74783	Herbicida	347	7	0.9	410	5	ABP30545	Streptoco
275	7	0.9	315	5	ABN91630	Herbicida	348	7	0.9	410	8	ADV83187	Streptoco
276	7	0.9	318	6	ABM67272	Photorhab	349	7	0.9	410	8	ADV83187	Streptoco
277	7	0.9	320	2	AA933279	43 KD end	350	7	0.9	410	8	ADV81048	Streptoco
278	7	0.9	324	6	ABU48397	Protein e	351	7	0.9	411	8	ADS23906	Bacterial
279	7	0.9	324	6	ABU48397	Protein e	352	7	0.9	413	4	AAU41340	Propionib
280	7	0.9	325	4	AAW79630	Corynebac	353	7	0.9	413	6	ABM37859	Propionib
281	7	0.9	325	4	AAW79630	Corynebac	354	7	0.9	413	6	ABM37859	Propionib
282	7	0.9	327	5	ABM89542	Pseudomon	355	7	0.9	413	6	ABM94363	M. xanthu
283	7	0.9	327	5	ABM89542	Pseudomon	356	7	0.9	416	6	ABU42300	Protein e
284	7	0.9	327	5	ABM89542	Pseudomon	357	7	0.9	416	6	ABU42300	Protein e
285	7	0.9	328	5	ABU51082	Helicobac	358	7	0.9	417	4	ABG03334	Novel hum
286	7	0.9	329	3	AAW52512	Helicobac	359	7	0.9	418	5	ABP27080	Streptoco
287	7	0.9	335	5	AAU93075	Arabidops	360	7	0.9	420	4	AAW62035	P. furios
288	7	0.9	335	5	AAU93075	Arabidops	361	7	0.9	420	4	AAW62035	P. furios
289	7	0.9	336	8	AD127927	Murine pr	362	7	0.9	423	4	ABG28086	Novel hum
290	7	0.9	337	3	AAW96738	Streptoco	363	7	0.9	423	4	ABG28086	Novel hum
291	7	0.9	337	5	ABP26971	Streptoco	364	7	0.9	425	3	AA44389	Zea may
292	7	0.9	337	5	ABP26971	Streptoco	365	7	0.9	425	3	AA44389	Zea may
293	7	0.9	337	5	ABP26971	Streptoco	366	7	0.9	426	6	ABU21982	Bacterial
294	7	0.9	337	8	ABU46738	Protein e	367	7	0.9	426	6	ABU21982	Bacterial
295	7	0.9	337	8	ABU46738	Protein e	368	7	0.9	426	6	ABU21982	Bacterial
296	7	0.9	337	8	ABU46738	Protein e	369	7	0.9	426	6	ABU21982	Bacterial
297	7	0.9	337	8	ABU46738	Protein e	370	7	0.9	434	8	ADN24740	Bacterial
298	7	0.9	337	8	ABU46738	Protein e	371	7	0.9	436	5	ABU50710	Helicobac
299	7	0.9	337	9	ADY19066	PRO polyp	372	7	0.9	436	5	ABU50710	Helicobac
300	7	0.9	337	9	ADY19066	PRO polyp	373	7	0.9	437	5	AAW47762	RNA bindi
301	7	0.9	341	4	ABW65050	Drosophil	374	7	0.9	441	7	ADH86636	Enterococ
302	7	0.9	341	4	ABW65050	Drosophil	375	7	0.9	442	5	ABW72317	Rat prote
303	7	0.9	342	5	ADY19670	Human dru	376	7	0.9	444	4	AAU03821	G protein
304	7	0.9	342	5	ADY19670	Human dru	377	7	0.9	444	4	AAU03821	G protein
305	7	0.9	342	5	ADY19670	Human dru	378	7	0.9	444	4	AAU03821	G protein
306	7	0.9	342	5	ADY19670	Human dru	379	7	0.9	444	4	AAU03821	G protein
307	7	0.9	342	5	ADY19670	Human dru	380	7	0.9	444	4	AAU03821	G protein
308	7	0.9	342	5	ADY19670	Human dru	381	7	0.9	444	4	AAU03821	G protein
309	7	0.9	342	5	ADY19670	Human dru	382	7	0.9	444	4	AAU03821	G protein
310	7	0.9	342	5	ADY19670	Human dru	383	7	0.9	444	4	AAU03821	G protein
311	7	0.9	342	5	ADY19670	Human dru	384	7	0.9	444	4	AAU03821	G protein
312	7	0.9	342	5	ADY19670	Human dru	385	7	0.9	444	4	AAU03821	G protein
313	7	0.9	342	5	ADY19670	Human dru	386	7	0.9	444	4	AAU03821	G protein
314	7	0.9	342	5	ADY19670	Human dru	387	7	0.9	444	4	AAU03821	G protein
315	7	0.9	342	5	ADY19670	Human dru	388	7	0.9	444	4	AAU03821	G protein
316	7	0.9	342	5	ADY19670	Human dru	389	7	0.9	444	4	AAU03821	G protein

390	7	0.9	464	6	ABU14689	Abu14689 Protein e	463	7	0.9	590	8	ADU25434	Adu25434 L. acidop
391	7	0.9	464	7	ADC31497	Adc31497 Human nov	464	7	0.9	596	8	ADN99873	Adn99873 Novel hum
392	7	0.9	465	7	ABO80641	AbO80641 Pseudomon	465	7	0.9	596	8	ADN99872	Adn99872 Novel hum
393	7	0.9	465	9	ADY86239	Ady86239 B. napus	466	7	0.9	609	3	AY73487	Aay73487 Human sec
394	7	0.9	466	4	AAU62912	Aau62912 Propionib	467	7	0.9	614	6	ADA33217	Ada33217 Acinetoba
395	7	0.9	466	6	ABM59431	Abm59431 Propionib	468	7	0.9	614	8	ADH48376	Adh48376 Human KPP
396	7	0.9	469	8	ADS24348	AdS24348 Bacterial	469	7	0.9	619	8	ADN23202	Adn23202 Bacterial
397	7	0.9	472	3	AAB18420	Aab18420 Amino aci	470	7	0.9	620	2	AAR77275	Aar77275 ORC2 subu
398	7	0.9	473	6	ADA33992	Ada33992 Acinetoba	471	7	0.9	620	2	AAW22225	Aaw22225 S. cerevi
399	7	0.9	478	4	ABB66297	Abb66297 Drosophil	472	7	0.9	620	5	AAU82999	Aau82999 S. cerevi
400	7	0.9	478	5	ABR38839	AbR38839 A. niger	473	7	0.9	620	6	ABR53643	Abr53643 Protein s
401	7	0.9	482	4	ADM19812	Adm19812 Protein e	474	7	0.9	620	7	ADK64130	Adk64130 Disease t
402	7	0.9	485	5	ADJ33852	Adj33852 Protein o	475	7	0.9	621	7	ADN18789	Adn18789 Bacterial
403	7	0.9	490	2	AY33929	Ay33929 Leukotoxi	476	7	0.9	621	7	ABO70379	AbO70379 Pseudomon
404	7	0.9	490	6	ADA28694	Ada28694 Plasmid p	477	7	0.9	622	5	ABF61455	Abf61455 Human NF-
405	7	0.9	494	9	ABE27284	AbE27284 Pinus rad	478	7	0.9	622	6	ABR41026	Abr41026 Human MAP
406	7	0.9	497	4	AAU37751	Aau37751 Streptoco	479	7	0.9	623	4	AAW79912	Aam79912 Human pro
407	7	0.9	497	6	ABU01284	Abu01284 S. pneumo	480	7	0.9	623	4	AAW79913	Aam79913 Human pro
408	7	0.9	497	6	ABU45988	Abu45988 Protein e	481	7	0.9	625	8	ADSA4452	AdS44452 Bacterial
409	7	0.9	497	8	ADK48573	Adk48573 Streptoco	482	7	0.9	627	4	ABG18262	Abg18262 Novel hum
410	7	0.9	497	8	ADM92139	Adm92139 S. pneumon	483	7	0.9	628	4	ABG23677	Abg23677 Novel hum
411	7	0.9	504	8	ADR59097	Adr59097 Novel S.	484	7	0.9	632	5	AAO19378	Aao19378 Human NF-
412	7	0.9	504	9	AEA59967	Aea59967 Streptoco	485	7	0.9	632	5	ABP61456	Abp61456 Human pal
413	7	0.9	514	6	ABJ20237	Abj20237 Human IG	486	7	0.9	649	4	ABB61237	Abb61237 Drosophil
414	7	0.9	517	3	AY32390	Ay32390 Herpesvir	487	7	0.9	662	9	AEA24005	Aea24005 Human PRO
415	7	0.9	517	5	AAE23294	Aae23294 Human nec	488	7	0.9	662	9	ABU24491	Abu24491 Protein e
416	7	0.9	518	5	ABG77170	Abg77170 Prostata	489	7	0.9	665	4	AAW78876	Aam78876 Human pro
417	7	0.9	518	8	ADS29669	AdS29669 Bacterial	490	7	0.9	665	9	ADY17134	Ady17134 PRO polyp
418	7	0.9	518	6	ABU85769	Abu85769 Human pro	491	7	0.9	666	4	AAW79657	Aaw79657 Corynebac
419	7	0.9	521	6	ABU35710	Abu35710 Protein e	492	7	0.9	666	4	AAU71885	Aau71885 C. glutam
420	7	0.9	522	6	ABU22090	Abu22090 Protein e	493	7	0.9	667	4	ABG16901	Abg16901 Novel hum
421	7	0.9	527	6	ABU19551	Abu19551 Protein e	494	7	0.9	667	4	AAU32908	Aau32908 Novel hum
422	7	0.9	528	4	ABW71669	Abw71669 Drosophil	495	7	0.9	671	2	AAW38505	Aaw38505 Streptoco
423	7	0.9	529	7	ADC61129	Adc61129 Baeyer-Vi	496	7	0.9	671	2	AAW85917	Aay85917 S. pneumo
424	7	0.9	529	8	ADT59473	Adt59473 Plant pol	497	7	0.9	671	8	ADK47127	Adk47127 Streptoco
425	7	0.9	531	8	ADP30594	Adp30594 Human sec	498	7	0.9	673	5	AAE25082	Aae25082 Human kin
426	7	0.9	531	8	ADP31696	Adp31696 Human sec	499	7	0.9	676	8	ADR95463	Adr95463 Novel S.
427	7	0.9	544	2	AAW03943	Aaw03943 LKT-GnRH	500	7	0.9	676	9	AEA59333	Aea59333 Streptoco
428	7	0.9	544	2	AAW79570	Aaw79570 LKT-GnRH	501	7	0.9	686	6	ABU39853	Abu39853 Protein e
429	7	0.9	549	3	ADM70886	Adm70886 Aspergill	502	7	0.9	692	8	ADN26147	Adn26147 Bacterial
430	7	0.9	549	9	ADZ64458	Adz64458 Human can	503	7	0.9	695	2	AAW79573	Aaw79573 LKT-GnRH
431	7	0.9	551	8	ADO65217	Ado65217 Novel hum	504	7	0.9	695	3	AAW58361	Aay58361 Leukotoxi
432	7	0.9	559	7	ABO75946	AbO75946 Pseudomon	505	7	0.9	695	3	AAW58133	Aay58133 Gonadotro
433	7	0.9	560	4	AAW78929	Aam78929 Human pro	506	7	0.9	699	7	ABO68327	AbO68327 Pseudomon
434	7	0.9	562	4	ABB64878	Abb64878 Drosophil	507	7	0.9	702	5	ABP65679	Abp65679 Bifidobac
435	7	0.9	564	6	ABJ37094	Abj37094 Low-affin	508	7	0.9	705	4	AAW79860	Aam79860 Human pro
436	7	0.9	564	8	ADT59636	Adt59636 Plant pol	509	7	0.9	705	8	ADP30746	Adp30746 Human sec
437	7	0.9	566	6	AAE35922	Aae35922 Human All	510	7	0.9	710	8	ADX77146	Adx77146 Plant ful
438	7	0.9	568	5	ABU51967	Abu51967 Helicobac	511	7	0.9	711	8	ADX92237	Adx92237 Plant ful
439	7	0.9	568	5	ABP74083	Abp74083 Candida a	512	7	0.9	717	4	ABB61609	Abb61609 Drosophil
440	7	0.9	572	6	ABJ37095	Abj37095 Low-affin	513	7	0.9	717	8	ADO07924	Ado07924 Fly polyp
441	7	0.9	572	7	ADC07800	Adc07800 Rice prot	514	7	0.9	731	5	ABU52070	Abu52070 Helicobac
442	7	0.9	572	7	ADF74126	Adf74126 Human nov	515	7	0.9	741	6	ABU42146	Abu42146 Protein e
443	7	0.9	573	4	ABB60673	Abb60673 Drosophil	516	7	0.9	742	9	ADZ64457	Adz64457 Human can
444	7	0.9	576	7	ABO74500	AbO74500 Pseudomon	517	7	0.9	745	9	AEA26999	Aea26999 Stress to
445	7	0.9	578	8	ADP03592	Adp03592 Infection	518	7	0.9	759	7	ABM88120	Abm88120 Rice abio
446	7	0.9	579	4	ABG24250	Abg24250 Novel hum	519	7	0.9	761	5	ABW77431	Abw77431 Human tum
447	7	0.9	580	5	AAAG66008	Aag66008 F. necrop	520	7	0.9	792	4	ABG15703	Abg15703 Novel hum
448	7	0.9	580	8	ADO47877	Ado47877 Alpha-Her	521	7	0.9	792	7	ABM85854	Abm85854 Mouse pro
449	7	0.9	581	8	ADP03590	Adp03590 Infection	522	7	0.9	792	8	ADH12911	Adh12911 Francisel
450	7	0.9	584	6	ABU19765	Abu19765 Protein e	523	7	0.9	797	8	ADS23447	AdS23447 Bacterial
451	7	0.9	587	4	AAW78928	Aam78928 Human pro	524	7	0.9	799	3	AAW92061	Aay92061 Human APC
452	7	0.9	587	5	AAU82982	Aau82982 Human hom	525	7	0.9	809	2	AAW29672	Aay29672 Human cer
453	7	0.9	587	5	AAU10799	Aau10799 Polymorph	526	7	0.9	816	8	ADP31581	Adp31581 Human sec
454	7	0.9	587	5	AAU10796	Aau10796 Reference	527	7	0.9	818	4	ABG92737	Aag92737 C glutami
455	7	0.9	587	5	AAU10797	Aau10797 Polymorph	528	7	0.9	821	7	ABO72267	AbO72267 Pseudomon
456	7	0.9	587	5	AAU10798	Aau10798 Polymorph	529	7	0.9	823	4	ABB71484	Abb71484 Drosophil
457	7	0.9	587	8	ADL17020	Adl17020 Human Ran	530	7	0.9	827	7	ADF06140	Adf06140 Bacterial
458	7	0.9	587	8	ADQ88017	Adq88017 Human Ran	531	7	0.9	850	4	ABBS2809	Abbs2809 Escherich
459	7	0.9	587	8	ABM82366	Abm82366 Tumour-as	532	7	0.9	861	8	ADP31340	Adp31340 Human sec
460	7	0.9	587	9	ADY19712	Ady19712 PRO polyp	533	7	0.9	870	8	ADP30646	Adp30646 Human sec
461	7	0.9	587	9	ADY16715	Ady16715 PRO polyp	534	7	0.9	874	6	ABU33564	Abu33564 Protein e
462	7	0.9	589	7	ADB85263	Abd85263 Mouse RNA	535	7	0.9	892	8	ADP31578	Adp31578 Human sec

536	7	0.9	897	4	ABB62261	Abb2261 Drosophil	609	7	0.9	1132	7	ADD71144	Add71144 Human int
537	7	0.9	908	6	ABU08492	Abu08492 Alpha-hel	610	7	0.9	1136	6	ABU08605	Abu08605 Neisseria
538	7	0.9	914	6	ABU08604	Abu08604 Neisseria	611	7	0.9	1139	6	ABG97360	Abg97360 Human CGD
539	7	0.9	921	2	AAW72033	Aaw72033 Hsv-2 str	612	7	0.9	1156	3	AB10104	Ab10104 Feline fcd
540	7	0.9	921	9	ABE37187	Aeb37187 L. pneumo	613	7	0.9	1161	5	ABG97354	Abg97354 Human CGD
541	7	0.9	921	9	ABE40526	Aeb40526 L. pneumo	614	7	0.9	1168	9	ADZ64454	Adz64454 Human can
542	7	0.9	924	2	AAW10889	Aar10889 Leukotoxi	615	7	0.9	1178	6	ABU08603	Abu08603 Neisseria
543	7	0.9	924	2	AAW10889	Aar10889 Leukotoxi	616	7	0.9	1187	8	ADP31342	Adp31342 Human sec
544	7	0.9	924	2	AAW10889	Aar10889 Leukotoxi	617	7	0.9	1197	8	AAE22860	Aae22860 Human pho
545	7	0.9	924	2	AAW10889	Aar10889 Leukotoxi	618	7	0.9	1216	5	AAE22860	Aae22860 Human pho
546	7	0.9	924	2	AAW10889	Aar10889 Leukotoxi	619	7	0.9	1268	4	ABB61314	Abb61314 Drosophil
547	7	0.9	926	2	AAW10889	Aar10889 Leukotoxi	620	7	0.9	1296	2	ADP31500	Adp31500 Human sec
548	7	0.9	926	2	AAW10889	Aar10889 Leukotoxi	621	7	0.9	1320	5	AAW10889	Aar10889 Leukotoxi
549	7	0.9	926	2	AAW10889	Aar10889 Leukotoxi	622	7	0.9	1334	2	AAW10889	Aar10889 Leukotoxi
550	7	0.9	926	2	AAW10889	Aar10889 Leukotoxi	623	7	0.9	1334	2	AAW10889	Aar10889 Leukotoxi
551	7	0.9	926	2	AAW10889	Aar10889 Leukotoxi	624	7	0.9	1334	2	AAW10889	Aar10889 Leukotoxi
552	7	0.9	926	2	AAW10889	Aar10889 Leukotoxi	625	7	0.9	1336	7	AAW10889	Aar10889 Leukotoxi
553	7	0.9	932	8	ADM08677	Adm08677 Human pro	626	7	0.9	1372	9	ADZ64453	Adz64453 Human can
554	7	0.9	933	8	ADM08677	Adm08677 Human pro	627	7	0.9	1380	9	ADZ64452	Adz64452 Human can
555	7	0.9	933	8	ADM08677	Adm08677 Human pro	628	7	0.9	1390	6	ABP60436	Abp60436 Human and
556	7	0.9	933	8	ADM08677	Adm08677 Human pro	629	7	0.9	1390	9	ADW02021	Adw02021 Human MPT
557	7	0.9	934	2	AAW07637	Aaw07637 P. suis 1	630	7	0.9	1390	9	ADY17478	Ady17478 PRO poly
558	7	0.9	937	8	ADH13664	Adh13664 Human ENZ	631	7	0.9	1390	9	ADY17963	Ady17963 PRO poly
559	7	0.9	937	8	ADH13664	Adh13664 Human ENZ	632	7	0.9	1396	8	ADN01130	Adn01130 Human cel
560	7	0.9	939	9	ADZ64455	Adz64455 Human can	633	7	0.9	1403	2	AAW10890	Aaw10890 lktA::lac
561	7	0.9	949	4	ABE68553	Ab68553 Human GTP	634	7	0.9	1403	2	AAW10890	Aaw10890 lktA::lac
562	7	0.9	950	4	ABE68553	Ab68553 Human GTP	635	7	0.9	1403	2	AAW10890	Aaw10890 lktA::lac
563	7	0.9	951	2	AAW34548	Aar34548 Rotavirus	636	7	0.9	1419	5	ABU65081	Abu65081 Human NOV
564	7	0.9	951	2	AAW34548	Aar34548 Rotavirus	637	7	0.9	1419	5	ABU65081	Abu65081 Human NOV
565	7	0.9	951	4	AAW79261	Aar79261 Human pro	638	7	0.9	1423	8	ADN61817	Adn61817 Human lip
566	7	0.9	953	2	AAW07167	Aar07167 105KD PTX	639	7	0.9	1423	8	ADN61817	Adn61817 Human lip
567	7	0.9	953	2	AAW15159	Aar15159 Leukotoxi	640	7	0.9	1423	8	ADN61817	Adn61817 Human lip
568	7	0.9	953	2	AAW15159	Aar15159 Leukotoxi	641	7	0.9	1433	8	ADO18815	Ado18815 Human NOV
569	7	0.9	953	2	AAW60072	Aar60072 FtxA prot	642	7	0.9	1434	2	AAW94380	Aaw94380 Mouse pat
570	7	0.9	953	2	AAW60072	Aar60072 FtxA prot	643	7	0.9	1434	2	AAW52199	Aaw52199 Mouse pat
571	7	0.9	956	6	ABU08602	Abu08602 Neisseria	644	7	0.9	1434	2	AAW72968	Aaw72968 Mouse pat
572	7	0.9	963	7	ADB67089	Adb67089 Kinesin h	645	7	0.9	1434	4	AAW67159	Aaw67159 Murine pa
573	7	0.9	963	7	ADB67091	Adb67091 Kinesin h	646	7	0.9	1434	4	AAW67159	Aaw67159 Murine pa
574	7	0.9	963	9	ABE08391	Aeb08391 c-Jun inh	647	7	0.9	1434	5	AAW67159	Aaw67159 Murine pa
575	7	0.9	964	8	ADL99362	Adl99362 Nanostroc	648	7	0.9	1434	7	ABU62271	Abu62271 Mouse pat
576	7	0.9	964	8	ADL99362	Adl99362 Nanostroc	649	7	0.9	1434	7	ABU62271	Abu62271 Mouse pat
577	7	0.9	964	8	ADL99362	Adl99362 Nanostroc	650	7	0.9	1434	7	ABU62271	Abu62271 Mouse pat
578	7	0.9	967	6	AAW80245	Aaw80245 Human lip	651	7	0.9	1434	8	ADE48980	Ade48980 Mouse pat
579	7	0.9	969	6	AAW34448	Aaw34448 Human lip	652	7	0.9	1439	4	AAU27557	Aau27557 Neisseria
580	7	0.9	977	2	AAW03942	Aaw03942 LKT-GnRH	653	7	0.9	1447	2	AAW75375	Aaw75375 Human pat
581	7	0.9	977	2	AAW03942	Aaw03942 LKT-GnRH	654	7	0.9	1447	2	AAW75375	Aaw75375 Human pat
582	7	0.9	978	7	ADM05468	Adm05468 Human pro	655	7	0.9	1447	2	AAW72969	Aaw72969 Human pat
583	7	0.9	979	9	ABE49457	Aeb49457 N. mening	656	7	0.9	1447	4	AAW67163	Aaw67163 Human pat
584	7	0.9	979	9	ABE49457	Aeb49457 N. mening	657	7	0.9	1447	5	AAE19830	Aae19830 Human pat
585	7	0.9	983	5	ABE77509	Ab77509 Tranetee	658	7	0.9	1447	5	ABJ10931	Abj10931 TRC8 rela
586	7	0.9	998	2	AAW38822	Aay38822 Neisseria	659	7	0.9	1447	5	AAW79571	Aaw79571 Human pat
587	7	0.9	1004	8	ADO18816	Ado18816 Human lip	660	7	0.9	1447	7	ABU62275	Abu62275 Human pat
588	7	0.9	1016	6	ABU41567	Abu41567 Protein e	661	7	0.9	1447	7	ADH62731	Adh62731 Human pat
589	7	0.9	1016	6	ABU41567	Abu41567 Protein e	662	7	0.9	1447	7	ADH62731	Adh62731 Human pat
590	7	0.9	1017	8	ADP31268	Adp31268 Human sec	663	7	0.9	1447	8	ADE48989	Ade48989 Human pat
591	7	0.9	1019	8	ADP31268	Adp31268 Human sec	664	7	0.9	1449	2	AAW38824	Aaw38824 Neisseria
592	7	0.9	1050	8	ADP31376	Adp31376 Human sec	665	7	0.9	1449	6	ABU37787	Abu37787 Protein e
593	7	0.9	1054	5	ABW79311	Abw79311 Human ova	666	7	0.9	1449	9	ABE49461	Aeb49461 N. mening
594	7	0.9	1069	2	AAW52748	Aaw52748 Bovine IF	667	7	0.9	1449	9	ABE49461	Aeb49461 N. mening
595	7	0.9	1069	2	AAW13867	Aaw13867 Chimeric	668	7	0.9	1454	3	AAW56621	Aaw56621 Neisseria
596	7	0.9	1069	3	AAW21074	Aaw21074 Bovine ga	669	7	0.9	1454	3	AAW38823	Aaw38823 Neisseria
597	7	0.9	1076	5	ABE69070	Ab69070 Human pol	670	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
598	7	0.9	1078	4	ABW61597	Abw61597 Drosophil	671	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
599	7	0.9	1088	4	AAW78676	Aaw78676 Human pro	672	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
600	7	0.9	1098	2	AAW22103	Aar22103 Bovine IL	673	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
601	7	0.9	1098	2	AAW22103	Aar22103 Bovine IL	674	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria
602	7	0.9	1098	2	AAW13866	Aaw13866 Chimeric	675	7	0.9	1457	6	ABU08601	Abu08601 Neisseria
603	7	0.9	1098	3	AAW21073	Aaw21073 Bovine IL	676	7	0.9	1457	6	ABU08601	Abu08601 Neisseria
604	7	0.9	1116	8	ADP31692	Adp31692 Human sec	677	7	0.9	1458	5	ABW09556	Abw09556 Human lip
605	7	0.9	1121	5	AAE20419	Aae20419 Human cdc	678	7	0.9	1458	5	ABW09556	Abw09556 Human lip
606	7	0.9	1121	5	AAE20419	Aae20419 Human cdc	679	7	0.9	1458	6	AAE34440	Aae34440 Human lip
607	7	0.9	1129	7	ABO79806	Ab79806 Pseudomon	680	7	0.9	1464	8	ADP31437	Adp31437 Human sec
608	7	0.9	1132	2	AAW77417	Aaw77417 Human cel	681	7	0.9	1468	2	AAW38825	Aaw38825 Neisseria

682	7	0.9	1468	6	ABP77279	Abp77279 N. gonorr	755	6	0.8	9	5	ABB95084	Abb95084 CTL epit
683	7	0.9	1468	6	ABU37103	Abu37103 Protein e	756	6	0.8	9	5	ABB94690	Abb94690 CTL epit
684	7	0.9	1468	9	ADV99673	Adv99673 Neisseria	757	6	0.8	9	5	AAO21237	Aao21237 Absorptio
685	7	0.9	1468	9	AEb49463	Aeb49463 N. gonorr	758	6	0.8	9	8	ADP25609	Adp25609 Plasmodiu
686	7	0.9	1628	4	ABG02195	Abg02195 Novel hum	759	6	0.8	9	9	AD250442	Ad250442 Y. pestis
687	7	0.9	1633	9	ABM93693	Abm93693 M. xanthu	760	6	0.8	9	9	AD281870	Ad281870 Human lam
688	7	0.9	1686	2	AAW70991	Aaw70991 Human cla	761	6	0.8	10	2	AAR33824	Aar33824 Selectin
689	7	0.9	1686	6	ABJ19811	Abj19811 Androgen-	762	6	0.8	10	2	AAR33825	Aar33825 Selectin
690	7	0.9	1725	8	ADP30654	Adp30654 Human sec	763	6	0.8	10	2	AAR33833	Aar33833 Selectin
691	7	0.9	1833	6	ADP30642	Adp30642 Human sec	764	6	0.8	10	2	AAR33834	Aar33834 Selectin
692	7	0.9	1846	6	ABR39833	AbR39833 Human SCA	765	6	0.8	10	2	AAR50817	Aar50817 Cyclic pe
693	7	0.9	1895	2	AAW72095	Aaw72095 HSV-2 str	766	6	0.8	10	4	AAG94318	Aag94318 Human com
694	7	0.9	1912	7	ADC26223	Adc26223 Human NOV	767	6	0.8	10	4	AAG85396	Aag85396 Saccharom
695	7	0.9	1943	6	ABU30826	Abu30826 Protein e	768	6	0.8	10	4	AAG85682	Aag85682 Saccharom
696	7	0.9	1956	8	ADN00371	Adn00371 Novel hum	769	6	0.8	10	5	ABB95044	Abb95044 CTL epit
697	7	0.9	1956	8	AEB13352	Aeb13352 KTAAL000	770	6	0.8	10	5	ABB94737	Abb94737 CTL epit
698	7	0.9	1974	2	AAW98391	Aaw98391 H. pylori	771	6	0.8	10	5	ABB94739	Abb94739 CTL epit
699	7	0.9	1984	4	ABG01338	Abg01338 Novel hum	772	6	0.8	10	5	ABB94944	Abb94944 CTL epit
700	7	0.9	2223	8	ADV99896	Adv99896 Nanchangm	773	6	0.8	10	5	ABB94629	Abb94629 CTL epit
701	7	0.9	2274	4	AAB50674	Aab50674 Mouse APC	774	6	0.8	10	8	ADK06129	Adk06129 Hepatitis
702	7	0.9	2274	8	ADO08047	Ado08047 Mouse pol	775	6	0.8	11	9	ADV14170	Adv14170 Yeast N-t
703	7	0.9	2274	8	ADZ85091	Adz85091 Full-leng	776	6	0.8	12	2	AAV21275	Aav21275 Human sem
704	7	0.9	2303	6	ABR58648	AbR58648 Human can	777	6	0.8	12	6	ABP98955	Abp98955 ErbB2 cel
705	7	0.9	2303	8	ADO08045	Ado08045 Human pol	778	6	0.8	12	9	AD281833	Ad281833 Human lam
706	7	0.9	2303	8	ADV70185	Adv70185 Tumor-ass	779	6	0.8	12	9	AEA18385	Aea18385 Peptide u
707	7	0.9	2338	8	ABo58348	Abo58348 Human gen	780	6	0.8	13	2	AAW23015	Aaw23015 R4 recept
708	7	0.9	2349	8	ADP30959	Adp30959 Human sec	781	6	0.8	13	6	ABP98589	Abp98589 Beta-barr
709	7	0.9	2382	8	ADP31341	Adp31341 Human sec	782	6	0.8	14	4	ABB56739	Abb56739 Human SNP
710	7	0.9	2431	2	AAW25138	Aar25138 SPV4 non-	783	6	0.8	15	5	ABP46959	Abp46959 Human Bly
711	7	0.9	2732	4	ABB52855	Abb52855 Escherich	784	6	0.8	15	7	ADF32583	Adf32583 Clostridi
712	7	0.9	2834	5	ABG97576	Abg97576 Haemagglu	785	6	0.8	15	7	ADG97786	Adg97786 scFV VHCD
713	7	0.9	2834	5	ADH80652	Adh80652 Escherich	786	6	0.8	15	9	ADW10966	Adw10966 Human pho
714	7	0.9	3119	2	AAW72204	Aaw72204 HSV-2 str	787	6	0.8	16	9	ADV13047	Adv13047 Human pho
715	7	0.9	3122	7	ADG75178	Adg75178 Human her	788	6	0.8	18	2	AAW40133	Aar40133 Delta'S s
716	7	0.9	3122	7	ADG75129	Adg75129 Human her	789	6	0.8	18	2	AAW36080	E. coli D
717	7	0.9	3194	6	ABU31122	Abu31122 Protein e	790	6	0.8	18	8	ADL15120	E. coli D
718	7	0.9	3194	9	ABE91380	Aeb91380 Microbial	791	6	0.8	18	9	ADZ11758	E. coli D
719	7	0.9	3339	8	ADP31219	Adp31219 Human sec	792	6	0.8	19	2	AAW46341	Aaw46341 Amino aci
720	7	0.9	3407	8	ADP31060	Adp31060 Human sec	793	6	0.8	19	5	ABBO7414	Aao07414 Plasmid p
721	7	0.9	3407	8	ADP31062	Adp31062 Human sec	794	6	0.8	19	5	AAO19110	Aao19110 Human cir
722	7	0.9	3455	8	ADP99914	Adp99914 Nanchangm	795	6	0.8	20	2	AAW22332	HIV-1 cli
723	7	0.9	3477	8	ADP30704	Adp30704 Human sec	796	6	0.8	20	2	AAW62895	Peptide s
724	7	0.9	3579	8	ADP31098	Adp31098 Human sec	797	6	0.8	21	3	AAV56865	B. catarr
725	7	0.9	3956	8	ADV99898	Adv99898 Nanchangm	798	6	0.8	21	3	AAV56865	B. catarr
726	7	0.9	4106	4	ABG99872	Abg99872 S. cinna	799	6	0.8	21	7	ADC73122	Domain l1
727	7	0.9	4752	8	ADP30585	Adp30585 Human sec	800	6	0.8	22	4	AAAB3929	Aab83929 Antigenic
728	7	0.9	4752	8	ADP30651	Adp30651 Human sec	801	6	0.8	23	6	ADA11828	Ada11828 Human nov
729	7	0.9	4999	5	AAO22158	Aao22158 Ramoplani	802	6	0.8	23	9	AD2866384	Ad2866384 Protein q
730	7	0.9	5304	8	ADP30706	Adp30706 Human sec	803	6	0.8	23	9	ABE25314	Aeb25314 Synthetic
731	7	0.9	6465	8	ADP30705	Adp30705 Human sec	804	6	0.8	23	9	ABE25313	Aeb25313 Synthetic
732	7	0.9	8026	6	AAE35489	Aae35489 Streptomy	805	6	0.8	24	5	AAU73141	Aau73141 Parathyro
733	7	0.9	8976	8	ADP31425	Adp31425 Human sec	806	6	0.8	24	5	AAU73142	Aau73142 Parathyro
734	7	0.9	9195	8	ADP31494	Adp31494 Human sec	807	6	0.8	24	8	ADQ75456	Adq75456 PTH/PTHrP
735	7	0.9	10944	8	ADP31311	Adp31311 Human sec	808	6	0.8	24	8	ADQ75457	Adq75457 PTH/PTHrP
736	7	0.9	11328	8	ADP31310	Adp31310 Human sec	809	6	0.8	25	9	ADV16640	Adv16640 E. faecal
737	7	0.9	36946	9	ADV97835	Adv97835 Murine pr	810	6	0.8	26	4	AAW99735	Aam99735 Human exc
738	6	0.8	6	4	AAU03972	Aau03972 Neisseria	811	6	0.8	26	4	AAW42550	Aam42550 Human kid
739	6	0.8	6	4	AAU03989	Aau03989 Neisseria	812	6	0.8	26	9	ABE25322	Aeb25322 Synthetic
740	6	0.8	6	4	AAU04415	Aau04415 Neisseria	813	6	0.8	28	2	AAW54400	Aaw54400 MAGE-10 t
741	6	0.8	6	4	AAU03962	Aau03962 Neisseria	814	6	0.8	28	3	AAV65042	Aay65042 Human 5'
742	6	0.8	6	4	AAU03968	Aau03968 Neisseria	815	6	0.8	28	3	AAV99875	Aay99875 Human MAG
743	6	0.8	6	4	AAU04431	Aau04431 Neisseria	816	6	0.8	28	4	AAQ13828	Aao13828 Human pol
744	6	0.8	6	4	AAU03983	Aau03983 Neisseria	817	6	0.8	28	5	AAU73105	Aau73105 Parathyro
745	6	0.8	7	2	AAW44781	Aar44781 Sequence	818	6	0.8	28	5	AAU73106	Aau73106 Parathyro
746	6	0.8	7	2	AAW44782	Aar44782 Sequence	819	6	0.8	28	8	ADQ75421	Adq75421 PTH/PTHrP
747	6	0.8	7	4	ABE62826	Aab62826 Fibrinoge	820	6	0.8	28	8	ADQ75420	Adq75420 PTH/PTHrP
748	6	0.8	7	4	ABE62823	Aab62823 Fibrinoge	821	6	0.8	28	9	ADU72606	Adu72606 Signal pe
749	6	0.8	7	5	AAO21220	Aao21220 Absorptio	822	6	0.8	28	9	ADZ73597	Adz73597 Human inc
750	6	0.8	8	2	AAW73428	Aar73428 Human TSH	823	6	0.8	29	6	ABJ26817	Abj26817 Endotheli
751	6	0.8	8	5	AAO21222	Aao21222 Absorptio	824	6	0.8	30	5	ABP29400	Abp29400 Streptoco
752	6	0.8	9	2	AAV25260	Aay25260 HIV Env g	825	6	0.8	30	5	AAU73170	Aau73170 Parathyro
753	6	0.8	9	5	ABB94918	Abb94918 CTL epit	826	6	0.8	30	5	AAU73136	Aau73136 Parathyro
754	6	0.8	9	5	ABB94587	Abb94587 CTL epit	827	6	0.8	30	5	AAU73137	Aau73137 Parathyro

828	6	0.8	30	8	ADQ75451	Adq75451 PTH/PTHrP	901	6	0.8	40	5	AAE25415	Aae25415 ZYMW AGII
829	6	0.8	30	8	ADQ75485	Adq75485 PTH/PTHrP	902	6	0.8	40	8	ADS05943	Ads05943 Staphyloc
830	6	0.8	30	8	ADQ75452	Adq75452 PTH/PTHrP	903	6	0.8	41	2	AY85919	AY85919 S. pneumo
831	6	0.8	31	2	AA04222	AA04222 Human par	904	6	0.8	41	2	AAU01637	AAU01637 Human PS2
832	6	0.8	31	2	AB57410	Ab57410 Human sec	905	6	0.8	42	4	AAU14818	AAU14818 Novel bon
833	6	0.8	31	5	AD124798	Adi24798 Parathyro	906	6	0.8	43	4	AAE04543	Aae04543 Pacific o
834	6	0.8	32	3	AY58650	AY58650 Calluna v	907	6	0.8	44	2	AAAR42290	AAr42290 Pestatin
835	6	0.8	32	3	AB333972	Ab333972 Human sec	908	6	0.8	44	2	AAAR87212	AAr87212 Restin de
836	6	0.8	32	3	AB333972	Ab333972 Human sec	909	6	0.8	44	3	AAAB16864	AAb16864 Bacteriop
837	6	0.8	32	3	AY44807	AY44807 Calluna v	910	6	0.8	44	3	AAAB53554	AAb53554 Human col
838	6	0.8	32	4	AB60746	Ab60746 Human sec	911	6	0.8	44	5	ADH32400	Adh32400 Yeast smo
839	6	0.8	33	2	AAAR80170	AAr80170 MiSP1-der	912	6	0.8	46	6	ABU00665	ABu00665 Human imm
840	6	0.8	33	4	AAAM16134	AAm16134 Peptide #	913	6	0.8	46	6	ABU00068	ABu00068 Human nov
841	6	0.8	33	4	AAAM28628	AAm28628 Peptide #	914	6	0.8	47	2	AAAR80176	AAr80176 MiSP1-der
842	6	0.8	33	4	AAAM83228	AAm83228 Human imm	915	6	0.8	47	2	AAAR80178	AAr80178 MiSP1-der
843	6	0.8	33	4	AB229945	Ab229945 Peptide #	916	6	0.8	48	2	AAAR80172	AAr80172 MiSP1-der
844	6	0.8	33	4	AB220544	Ab220544 Protein #	917	6	0.8	48	2	AAAR80178	AAr80178 MiSP1-der
845	6	0.8	33	4	AAAM68319	AAm68319 Human bon	918	6	0.8	48	7	ADA49395	ADa49395 Lymphaden
846	6	0.8	33	4	ABG49983	ABg49983 Human liv	919	6	0.8	49	2	AAAR80173	AAr80173 MiSP1-der
847	6	0.8	33	4	AAAM03864	AAm03864 Peptide #	920	6	0.8	49	3	AAAG12570	AAg12570 Zea may
848	6	0.8	33	5	ABG77069	ABg77069 Prostata	921	6	0.8	49	8	ADL97663	ADl97663 Protein e
849	6	0.8	33	5	ABG37869	ABg37869 Human pep	922	6	0.8	50	2	AAAR80179	AAr80179 MiSP1-der
850	6	0.8	33	8	ABO59958	ABo59958 Human gen	923	6	0.8	50	2	AAAR89339	AAr89339 Salmonell
851	6	0.8	34	2	AAAR45483	AAr45483 Parathyro	924	6	0.8	50	5	ABP06117	ABp06117 Human ORF
852	6	0.8	34	2	AAAR69009	AAr69009 PTH analo	925	6	0.8	50	7	ABM74476	ABm74476 DNA clone
853	6	0.8	34	2	AAW13300	AAw13300 Truncated	926	6	0.8	51	2	AAAR80171	AAr80171 MiSP1-der
854	6	0.8	34	2	AAW12179	AAw12179 Parathyro	927	6	0.8	51	2	AAAR80182	AAr80182 MiSP1-der
855	6	0.8	34	2	AAW61677	AAw61677 Parathyro	928	6	0.8	51	4	ABBA2173	ABb42173 Peptide #
856	6	0.8	34	2	AAW65997	AAw65997 Parathyro	929	6	0.8	51	4	ABBA2863	ABb42863 Peptide #
857	6	0.8	34	2	AAW81893	AAw81893 Synthetic	930	6	0.8	51	4	AAAM35980	AAm35980 Peptide #
858	6	0.8	34	2	AAW74357	AAw74357 Modified	931	6	0.8	51	4	AAAM36677	AAm36677 Peptide #
859	6	0.8	34	3	AB38530	AB38530 Human sec	932	6	0.8	51	4	ABBA26136	ABb26136 Protein #
860	6	0.8	34	5	AAU73334	AAu73334 Parathyro	933	6	0.8	51	4	AAAM75869	AAm75869 Human bon
861	6	0.8	34	5	AAU73100	AAu73100 Parathyro	934	6	0.8	51	4	AAAM76570	AAm76570 Human bon
862	6	0.8	34	5	AAU73101	AAu73101 Parathyro	935	6	0.8	51	4	AAAM63756	AAm63756 Human bra
863	6	0.8	34	8	ABU42245	ABu42245 Protein e	936	6	0.8	51	4	AAAM63058	AAm63058 Human bra
864	6	0.8	34	8	ADH35573	ADh35573 Human par	937	6	0.8	51	4	ABG58269	ABg58269 Human liv
865	6	0.8	34	8	ADH35571	ADh35571 Human par	938	6	0.8	51	4	ABG57603	ABg57603 Human liv
866	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP	939	6	0.8	51	4	AAAG90451	AAg90451 C Glutami
867	6	0.8	34	8	ADQ75416	Adq75416 PTH/PTHrP	940	6	0.8	51	5	ABP02926	ABp02926 Human ORF
868	6	0.8	34	8	ADQ75449	Adq75449 PTH/PTHrP	941	6	0.8	51	5	ABG45818	ABg45818 Human pep
869	6	0.8	34	9	ABE51295	ABe51295 Human PTH	942	6	0.8	52	3	ABG426169	ABg426169 Rat GBX2
870	6	0.8	34	9	ABE51293	ABe51293 Human PTH	943	6	0.8	52	4	AAU52328	AAu52328 Novel hum
871	6	0.8	34	9	ABE70785	ABe70785 Human PTH	944	6	0.8	52	4	AAU52328	AAu52328 Propionib
872	6	0.8	34	9	ABE70787	ABe70787 Human PTH	945	6	0.8	52	6	ABM48847	ABm48847 Propionib
873	6	0.8	35	4	AAO13575	AAo13575 Human pol	946	6	0.8	52	6	ABM48847	ABm48847 Propionib
874	6	0.8	36	2	AAAM58185	AAm58185 [Lys18]-h	947	6	0.8	52	8	ABO59052	ABo59052 Human gen
875	6	0.8	36	4	AAAM15740	AAm15740 Peptide #	948	6	0.8	52	8	ADU02556	ADu02556 Novel hum
876	6	0.8	36	4	AAAM28249	AAm28249 Peptide #	949	6	0.8	53	7	ADF59117	ADf59117 Human pol
877	6	0.8	36	4	ABE29559	ABe29559 Peptide #	950	6	0.8	54	3	AAAB34069	AAb34069 Human sec
878	6	0.8	36	4	ABE20152	ABe20152 Protein #	951	6	0.8	54	8	ABP08116	ABp08116 Human ORF
879	6	0.8	36	4	AAAM67923	AAm67923 Human bon	952	6	0.8	54	8	ADT38445	ADt38445 hSARS vir
880	6	0.8	36	4	AAAM55539	AAm55539 Human liv	953	6	0.8	54	8	ADT38445	ADt38445 hSARS vir
881	6	0.8	36	4	ABG49566	ABg49566 Human liv	954	6	0.8	55	2	AAAR80177	AAr80177 MiSP1-der
882	6	0.8	36	4	AAAM03474	AAm03474 Peptide #	955	6	0.8	55	2	ABBA43693	ABb43693 Peptide #
883	6	0.8	36	9	ABM94818	ABm94818 M. xanthu	956	6	0.8	55	4	AAAM82838	AAm82838 Human imm
884	6	0.8	37	4	AAE00729	AAe00729 Homeodoma	957	6	0.8	55	4	AAAU0171	AAu0171 Propionib
885	6	0.8	37	4	AAAM14064	AAm14064 Peptide #	958	6	0.8	55	4	AAAU52709	AAu52709 Propionib
886	6	0.8	38	4	AB333009	AB333009 Peptide #	959	6	0.8	55	4	ABG59065	ABg59065 Human liv
887	6	0.8	38	4	AAAM26470	AAm26470 Peptide #	960	6	0.8	55	6	ABM36690	ABm36690 Propionib
888	6	0.8	38	4	AB27838	AB27838 Human pep	961	6	0.8	55	6	ABM49228	ABm49228 Propionib
889	6	0.8	38	4	ABBI8482	ABb18482 Protein #	962	6	0.8	55	6	ABM49228	ABm49228 Propionib
890	6	0.8	38	4	AAAM66193	AAm66193 Human bon	963	6	0.8	55	6	ABU56878	ABu56878 BoNT/A Hc
891	6	0.8	38	4	AAAM53807	AAm53807 Human bra	964	6	0.8	55	6	ABU56877	ABu56877 BoNT/A Hc
892	6	0.8	38	4	ABG47861	ABg47861 Human liv	965	6	0.8	56	2	AAAW77572	AAw77572 Staphyloc
893	6	0.8	38	4	AAAM01804	AAm01804 Peptide #	966	6	0.8	56	3	AAAB33881	AAb33881 Human sec
894	6	0.8	38	5	ABG35843	ABg35843 Human pep	967	6	0.8	56	4	AAAM19289	AAm19289 Peptide #
895	6	0.8	38	8	ADN46506	ADn46506 Thermococ	968	6	0.8	56	4	ABB38566	ABb38566 Peptide #
896	6	0.8	39	2	AAAR80174	AAr80174 MiSP1-der	969	6	0.8	56	4	AAAM32017	AAm32017 Peptide #
897	6	0.8	39	3	AAAY55704	AAy55704 M. genita	970	6	0.8	56	4	ABBA23694	ABb23694 Protein #
898	6	0.8	39	4	AAU21463	AAu21463 Human nov	971	6	0.8	56	4	AAAM71725	AAm71725 Human bon
899	6	0.8	39	8	ABO56803	ABo56803 Human gen	972	6	0.8	56	4	AAO10744	AAo10744 Human pol
900	6	0.8	40	2	AAAY85845	AAy85845 S. pneumo	973	6	0.8	56	4	AAAM59190	AAm59190 Human bra

974 6 0.8 56 4 ABG53410 Human liv
975 6 0.8 56 5 ABP10151 Human ORF
976 6 0.8 56 5 ABG41539 Human pep
977 6 0.8 57 2 AAY12580 Human 5'
978 6 0.8 57 4 AAM13734 Peptide #
979 6 0.8 57 4 ABB32669 Peptide #
980 6 0.8 57 4 AAM8987 Human imm
981 6 0.8 57 4 ABG47522 Human liv
982 6 0.8 58 4 AAB65135 Rat phys1
983 6 0.8 58 4 AAM89036 Human imm
984 6 0.8 58 4 AAU63871 Propionib
985 6 0.8 58 4 ABG22198 Novel hum
986 6 0.8 58 6 ABM60390 Propionib
987 6 0.8 58 8 ADW15853 ADAMS55 e
988 6 0.8 59 2 AAW26186 Fragment
989 6 0.8 59 4 ABB69382 Drosophi1
990 6 0.8 59 4 ABB28297 Human pep
991 6 0.8 59 4 AAM66647 Human bon
992 6 0.8 59 4 AAO12589 Human pol
993 6 0.8 59 4 AAU55699 Propionib
994 6 0.8 59 4 AAM54254 Human bra
995 6 0.8 59 6 ABM52218 Propionib
996 6 0.8 60 2 AAY05924 Thermophi
997 6 0.8 60 2 AAY45146 Rat ligan
998 6 0.8 60 4 AAM16802 Peptide #
999 6 0.8 60 4 AAB65132 Rat phys1
1000 6 0.8 60 4 AAG74452 Human col

ALIGNMENTS

RESULT 1
AAY84947
XX ID AAY84947 standard; protein; 797 AA.
AC AAY84947;
XX
DT 21-AUG-2000 (first entry)
XX
DE Amino acid sequence of outer membrane protein (omp) 85.
XX
KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
KW meningococcal infection; protective immune response; vaccine.
XX
OS Neisseria meningitidis.
XX
PN WO200023595-A1.
XX
PD 27-APR-2000.
XX
XX 22-OCT-1998; 98WO-US022352.
PF
XX 22-OCT-1998; 98WO-US022352.
PR
XX (UYMO-) UNIV MONTANA.
PA
XX Judd RC, Manning SD;
PI
XX WPI; 2000-339694/29.
DR N-PSDB; AAA15156.
XX
XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
PT meningitidis useful for vaccine, therapeutic and diagnostic compositions
PT for gonococcal or meningococcal infections.
XX
XX Claim 41; Page 89-92; 98pp; English.
XX
XX The present sequence represents an outer membrane protein (omp) 85 of
CC Neisseria meningitidis. The omp polypeptides and polynucleotides are
CC useful in compositions for use in the prevention, treatment and diagnosis
CC of non-symptomatic gonococcal infection or meningococcal infection and
CC symptomatic disease. They are also useful for the detection of

CC hybridisation complexes. Antigens and antibodies specific omp proteins
CC also provide diagnostic, therapeutic and prophylactic compositions for
CC the treatment or prevention of the infections described above. The
CC antibodies are useful for inducing a protective immune response in humans
CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC species. The proteins, antibodies and polynucleotide sequences of the
CC present invention may also be used in the screening and development of
CC chemical compounds such as drugs or vaccines
XX
SQ Sequence 797 AA;
Query Match 100.0%; Score 797; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKLKQIASALMLGSLPLAFADFTTQDIVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGSLPLAFADFTTQDIVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKWLQNDAIKQLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKWLQNDAIKQLESFGLAQ 120
Qy 121 SQYFNQATLNOAVAGLKEEYLGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNOAVAGLKEEYLGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
Qy 181 FEGNQVYSRKLQRQMSLTGEGGIWTLTRSNQFNEQKFAQDMKEKVTDFQNNGYDFPRIL 240
Db 181 FEGNQVYSRKLQRQMSLTGEGGIWTLTRSNQFNEQKFAQDMKEKVTDFQNNGYDFPRIL 240
Qy 241 DTDIQTNEDKTKOTIKITVHEGGRFHWKVSIEGDTNEVPKAELEKLLTWKPKWTEROQ 300
Db 241 DTDIQTNEDKTKOTIKITVHEGGRFHWKVSIEGDTNEVPKAELEKLLTWKPKWTEROQ 300
Qy 301 MTAVLGEIQNRMGSGAYSEISVQPLPNAETKTVDLHIEPGRKIYVNEIHTGNKT 360
Db 301 MTAVLGEIQNRMGSGAYSEISVQPLPNAETKTVDLHIEPGRKIYVNEIHTGNKT 360
Qy 361 RDEVVRRELQMESAPYDTSKLQSKVERVELLYGFDNVQFDAPVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQMESAPYDTSKLQSKVERVELLYGFDNVQFDAPVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGSLSFDPYFTA 480
Qy 481 DGVSGLGYDVYKAFDPKRAKSTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAFDPKRAKSTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHADFIKKYKTDGTSFGWLYKGTGVGRNKTDSALMPTTRGYLTVGNNAEIA 600
Db 541 YNKAPKHADFIKKYKTDGTSFGWLYKGTGVGRNKTDSALMPTTRGYLTVGNNAEIA 600
Qy 601 LPGSKLQYYSATHNQWTFPPLSKITFTMLGCEVGIAGGYGRTKEIPFFENFYGGGLSVR 660
Db 601 LPGSKLQYYSATHNQWTFPPLSKITFTMLGCEVGIAGGYGRTKEIPFFENFYGGGLSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAAELFFPMPGAADARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAAELFFPMPGAADARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGGAVTWLSPGPMKFRYAYPLKK 780
Db 721 KTYDDNSSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGGAVTWLSPGPMKFRYAYPLKK 780
Qy 781 KPDEIQRFOFQLGTTTF 797
Db 781 KPDEIQRFOFQLGTTTF 797
RESULT 2

XX WPI; 2005-272369/28.
DR N-PSDB; ADZ09416.
XX
PT New isolated nucleic acid encoding outer membrane protein 85 (Omp85) of
PT Neisseria gonorrhoeae or Neisseria meningitidis, useful for preventing,
PT treating, or diagnosing non-symptomatic gonococcal infection or
PT meningococcal infection.
XX
PS Claim 1; SEQ ID NO 4; 41bp; English.
XX
CC The invention relates to a nucleic acid molecule comprising: (a) the 2379
CC or 2394 bp sequence of ADZ09414 or ADZ09416; or (b) a sequence capable of
CC hybridizing to it, or its fragment, which when expressed in a host cell
CC produces the outer membrane protein Omp85 polypeptide which induces
CC antibodies to Neisseria gonorrhoeae or N. meningitidis, under the control
CC of suitable regulatory sequences which direct expression of the
CC polypeptide in the host cell. The nucleic acid and amino acid sequences
CC of the Omp85 protein of N. gonorrhoeae or N. meningitidis are useful as
CC vaccine compositions, therapeutic compositions, and diagnostic
CC compositions for preventing, treating, or diagnosing non-symptomatic
CC gonococcal infection or symptomatic disease and non-symptomatic
CC meningococcal infection or symptomatic disease. The present sequence
CC represents the N. meningitidis Omp85 protein. Note: the N. meningitidis
CC Omp85 protein is referred to the Genbank accession number AF021045, but
CC this number refers to the *Oncorhynchus kisutch* insulin-like growth factor
CC receptor-2 (SIR-6) mRNA, partial cds sequence.
XX
SQ Sequence 797 AA;

Query Match 100.0%; Score 797; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60

Qy 61 IIKSLYATGFFDVRVETADQQLLTVERPTTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120
Db 61 IIKSLYATGFFDVRVETADQQLLTVERPTTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120

Qy 121 SOYFNQATLQAVAGLKEEYLGKLNIOITPKVTKLARNRVIDITIDEGSAKITDIE 180
Db 121 SOYFNQATLQAVAGLKEEYLGKLNIOITPKVTKLARNRVIDITIDEGSAKITDIE 180

Qy 181 PEGNQVYSDRKLQMQLSTEGGIWTWLTTRSNQFNEQKFAQDMKVTFDYQNGYDFDPRIL 240
Db 181 PEGNQVYSDRKLQMQLSTEGGIWTWLTTRSNQFNEQKFAQDMKVTFDYQNGYDFDPRIL 240

Qy 241 DTDIQTWEDTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQ 300
Db 241 DTDIQTWEDTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQ 300

Qy 301 MTAVLGIEIQNRMSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
Db 301 MTAVLGIEIQNRMSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360

Qy 361 RDEVVRELROMESAPYDTSKLQSKERVLLGVDFNVQDPAVPLAGTDPKVDLNMSLTE 420
Db 361 RDEVVRELROMESAPYDTSKLQSKERVLLGVDFNVQDPAVPLAGTDPKVDLNMSLTE 420

Qy 421 RSTGSLDLSAGWQDVTGLVMSAGVSDNLFTGTGSAALRASRSKTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDLSAGWQDVTGLVMSAGVSDNLFTGTGSAALRASRSKTTLNGSLSFDPYFTA 480

Qy 481 DGVSGLGVDVYKAPDPKRASTSIKQYKTTTAGAGIRMSVPVTEYDRNFGVLAHLLTVNT 540
Db 481 DGVSGLGVDVYKAPDPKRASTSIKQYKTTTAGAGIRMSVPVTEYDRNFGVLAHLLTVNT 540

Qy 541 YNKAPKHVADPIKYGKTDGDSFGKWLKYGTGVGGRNKTDLSALWTRGYLTGVNAEIA 600
Db 541 YNKAPKHVADPIKYGKTDGDSFGKWLKYGTGVGGRNKTDLSALWTRGYLTGVNAEIA 600

Qy 601 LPGSKLOYYSATHNOTWFPPLSKTFTMLGSGEVGIAGGYGRTKEIPFFSNFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNOTWFPPLSKTFTMLGSGEVGIAGGYGRTKEIPFFSNFYGGGLGSVR 660

Qy 661 GYESGTLGPKVYDEYGEKISYGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720

Qy 721 KTYDDNSSSATGGRVONIYGAGNTHKSTFTNLRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSSATGGRVONIYGAGNTHKSTFTNLRYSAGGAVTWLSPLGPMKFRYAYPLKK 780

Qy 781 KPDEIQRFQFQLGTTTF 797
Db 781 KPDEIQRFQFQLGTTTF 797

RESULT 4
AAU03959
ID AAU03959 standard; protein; 797 AA.
XX
AC AAU03959;
XX
DT 23-OCT-2001 (first entry)
XX
DE Neisseria gonorrhoeae antigenic protein.
XX
KW Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.
XX
OS Neisseria gonorrhoeae.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /note= "Signal peptide"
FT Protein 22..797
FT /note= "Mature N. gonorrhoeae antigen"
XX
PN WO200138350-A2.
XX
PD 31-MAY-2001.
XX
PF 28-NOV-2000; 2000WO-IB001851.
XX
PR 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX
PA (CHIR-) CHIRON SPA.
PA (STAT-) STATENS INST FOLKEHELSE.
XX
PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX WPI; 2001-381289/40.
DR N-PSDB; AAS07279.
XX
DR Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX
PS Claim 1; Page 37-39; 92pp; English.
XX
CC The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.
CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the
CC pharynx, causing meningitis and, occasionally, septicaemia in the absence
CC of meningitis. This antigenic protein is useful in the manufacture of a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria, such as meningitis and septicaemia. It is also useful as a
CC diagnostic reagent for detecting the presence of Neisseria bacteria or
CC antibodies raised against Neisseria, and as a reagent for raising the
CC antibodies. The Neisserial nucleotide sequences can be expressed in a
CC variety of different expression systems, for example, mammalian cells,
CC baculoviruses, plants, bacteria and yeast

XX	SQ	Sequence 797 AA;	
		Query Match 94.4%; Score 752; DB 4; Length 797;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	21	ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80	
Db	21	ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80	
Qy	81	GQLLTWIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140	
Db	81	GQLLTWIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140	
Qy	141	LGRGKLNIIQITPKVTKLARNRVDITIDEKSAKITDIEPEGNOQVSDRKLQRMSLTE 200	
Db	141	LGRGKLNIIQITPKVTKLARNRVDITIDEKSAKITDIEPEGNOQVSDRKLQRMSLTE 200	
Qy	201	GGIWTWLTNRNQNFEQFAQDMKVTDYFQNNGYDFRILDTDIQTNEDEKTKQTIKIIVH 260	
Db	201	GGIWTWLTNRNQNFEQFAQDMKVTDYFQNNGYDFRILDTDIQTNEDEKTKQTIKIIVH 260	
Qy	261	EGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQTAVLGEIQNRMSGAGYAYS 320	
Db	261	EGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQTAVLGEIQNRMSGAGYAYS 320	
Qy	321	EISVQPLPNAETKTVDVFLHIETPGRKIYVNEIHITGNKKTDEVRRLQMESAPYDTS 380	
Db	321	EISVQPLPNAETKTVDVFLHIETPGRKIYVNEIHITGNKKTDEVRRLQMESAPYDTS 380	
Qy	381	KLQSKERVLLGYFDNVQFPAVPLAGTPDKVDLNMSLTERSTGSLDLISAGWVODTGLVM 440	
Db	381	KLQSKERVLLGYFDNVQFPAVPLAGTPDKVDLNMSLTERSTGSLDLISAGWVODTGLVM 440	
Qy	441	SAGVSQDNLFGTGSAALRASRKTLLNGSLSFDPYFTADGVSIGYDVYKGFDPKAS 500	
Db	441	SAGVSQDNLFGTGSAALRASRKTLLNGSLSFDPYFTADGVSIGYDVYKGFDPKAS 500	
Qy	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDG 560	
Db	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDG 560	
Qy	561	TDGSPKGLYKGTGCGRNKTDLSALWPTRGVLTGVAEIALPGSKLOVYSATHNQTFPP 620	
Db	561	TDGSPKGLYKGTGCGRNKTDLSALWPTRGVLTGVAEIALPGSKLOVYSATHNQTFPP 620	
Qy	621	LSKTFLLMGLGEGVGIAGVGRTKEIPFFENFYGGGLGSRVGYESTLGPVYDEYGEKIS 680	
Db	621	LSKTFLLMGLGEGVGIAGVGRTKEIPFFENFYGGGLGSRVGYESTLGPVYDEYGEKIS 680	
Qy	681	YGGNKKANVSARELLPFMPGAKDARTVRLSLPADAGSVMDGKTYDDNSSATGGRVQNIYG 740	
Db	681	YGGNKKANVSARELLPFMPGAKDARTVRLSLPADAGSVMDGKTYDDNSSATGGRVQNIYG 740	
Qy	741	AGNTHKSTFTNELRYSAGAVTWLSPLGPMKF 772	
Db	741	AGNTHKSTFTNELRYSAGAVTWLSPLGPMKF 772	
		RESULT 5	
		AAU03957	
ID	AAU03957	standard; protein; 797 AA.	
XX	XX		
AC	AAU03957;		
XX	23-OCT-2001	(first entry)	
DE	Neisseria meningitidis serogroup B antigenic protein.		
XX	Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;		
KW	bacterial infection; baculovirus; yeast.		
XX			

OS	Neisseria meningitidis.	
XX	Key	Location/Qualifiers
PH	Peptide	1..21
FT	Protein	/note="Signal peptide"
FT	Binding-site	715..722
XX		/note="ATP/GTP-binding site motif A (P-loop)"
PN	WO200138350-A2.	
XX	31-MAY-2001.	
XX	28-NOV-2000;	2000WO-IB001851.
XX	29-NOV-1999;	99GB-00028197.
PR	09-MAR-2000;	2000GB-00005698.
XX	(CHIR-) CHIRON SPA.	
PA	(STAT-) STATENS INST FOLKEHELSE.	
XX	Giuliani MM, Pizza M, Rappuoli R, Holst J;	
PI	WPI; 2001-381289/40.	
DR	N-PSDB; AAS07277.	
XX	Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection.	
PT	Claim 1; Fig 1; 92pp; English.	
PS	The sequence represents a Neisseria meningitidis serogroup B 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants, bacteria and yeast	
XX	Sequence 797 AA;	
SQ	Query Match 94.4%; Score 752; DB 4; Length 797;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	21	ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80
Db	21	ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80
Qy	81	GQLLTWIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Db	81	GQLLTWIERPTIGSLNITGAKMLQNDAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Qy	141	LGRGKLNIIQITPKVTKLARNRVDITIDEKSAKITDIEPEGNOQVSDRKLQRMSLTE 200
Db	141	LGRGKLNIIQITPKVTKLARNRVDITIDEKSAKITDIEPEGNOQVSDRKLQRMSLTE 200
Qy	201	GGIWTWLTNRNQNFEQFAQDMKVTDYFQNNGYDFRILDTDIQTNEDEKTKQTIKIIVH 260
Db	201	GGIWTWLTNRNQNFEQFAQDMKVTDYFQNNGYDFRILDTDIQTNEDEKTKQTIKIIVH 260
Qy	261	EGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQTAVLGEIQNRMSGAGYAYS 320
Db	261	EGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQTAVLGEIQNRMSGAGYAYS 320
Qy	321	EISVQPLPNAETKTVDVFLHIETPGRKIYVNEIHITGNKKTDEVRRLQMESAPYDTS 380
Db	321	EISVQPLPNAETKTVDVFLHIETPGRKIYVNEIHITGNKKTDEVRRLQMESAPYDTS 380

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Db 321 EISVQPLPNAETKTVDVFLHIEPRKIIYVNEIHIITGNKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQSKERVLLGYFDNVQFDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
| 381 KLQSKERVLLGYFDNVQFDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
| 381 KLQSKERVLLGYFDNVQFDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFPGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSIGVDYVYKAFDPRKAS 500
| 441 SAGVSQDNLFPGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSIGVDYVYKAFDPRKAS 500
| 441 SAGVSQDNLFPGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSIGVDYVYKAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG 560
| 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG 560
| 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG 560
Qy 561 TDGSFKGWLKYGTVGWRNKTTDSALWPTRGYLTVGNVNAEIALPGSKLQYYSATHNQWTFPP 620
| 561 TDGSFKGWLKYGTVGWRNKTTDSALWPTRGYLTVGNVNAEIALPGSKLQYYSATHNQWTFPP 620
| 561 TDGSFKGWLKYGTVGWRNKTTDSALWPTRGYLTVGNVNAEIALPGSKLQYYSATHNQWTFPP 620
Qy 621 LSKTFTLMLGGEVGIAGGYGRKTEIPEFFENFYGGGLSVRGYSGTGLGPKVYDEYGEKIS 680
| 621 LSKTFTLMLGGEVGIAGGYGRKTEIPEFFENFYGGGLSVRGYSGTGLGPKVYDEYGEKIS 680
| 621 LSKTFTLMLGGEVGIAGGYGRKTEIPEFFENFYGGGLSVRGYSGTGLGPKVYDEYGEKIS 680
Qy 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWMDGKTYDDNSSSATGGRVQNIY 740
| 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWMDGKTYDDNSSSATGGRVQNIY 740
| 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWMDGKTYDDNSSSATGGRVQNIY 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
| 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
| 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
```

RESULT 6

```
AAU04451
ID AAU04451 standard; protein; 797 AA.
XX AC AAU04451;
XX AC AAU04451;
XX DT 23-OCT-2001 (first entry)
XX DE Neisseria meningitidis serogroup A antigenic protein #2.
XX KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
XX KW bacterial infection; baculovirus; yeast.
XX OS Neisseria meningitidis.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein 22..797
XX FT /note= "Signal peptide"
XX FT /note= "Mature N. meningitidis serogroup A antigen"
XX PN WO200138350-A2.
XX PD 31-MAY-2001.
XX PF 28-NOV-2000; 2000WO-IB001851.
XX PR 29-NOV-1999; 99GB-00028197.
XX PR 09-MAR-2000; 2000GB-00005698.
XX PR (CHIR-) CHIRON SPA.
XX PA (STAT-) STATENS INST FOLKEHELSE.
XX PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX WPI; 2001-381289/40.
XX PT Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
XX PT gonorrhoeae, useful in the manufacture of a medicament for treating and
XX PT preventing Neisserial bacteria infection.
XX PS Claim 1; Page 39-40; 92pp; English.
```

```
XX CC The sequence represents a Neisseria meningitidis serogroup A 85 kDa
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicaemia in the absence of meningitis.
CC This antigenic protein is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast. Note: There are two versions of this sequence
CC displayed in the specification (see AAU03958)
```

XX SQ Sequence 797 AA;

```
Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 21 ADFTIODIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIODIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAIKSLYATGFFDDVRVETAD 80
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDALKKNLSEFGLAQSOYFNQATLNOAVAGLKEEY 140
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDALKKNLSEFGLAQSOYFNQATLNOAVAGLKEEY 140
Qy 141 LGRGKLNIQITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNQYVSDRKLQRMSLTE 200
Db 141 LGRGKLNIQITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNQYVSDRKLQRMSLTE 200
Qy 201 GGIWTLTRSNQFNEQKPAQDMKVTDFYQNNGYDFRILDTDIQNEKTKQTIKITH 260
Db 201 GGIWTLTRSNQFNEQKPAQDMKVTDFYQNNGYDFRILDTDIQNEKTKQTIKITH 260
Qy 261 EGGRFPMGKVSIEGDTNEVPKAELEKLLTMKPGKYEROQMTAVLGEIQNRMGSAAYAS 320
Db 261 EGGRFPMGKVSIEGDTNEVPKAELEKLLTMKPGKYEROQMTAVLGEIQNRMGSAAYAS 320
Qy 321 EISVQPLPNAETKTVDVFLHIEPRKIIYVNEIHIITGNKTRDEVVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPRKIIYVNEIHIITGNKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQSKERVLLGYFDNVQFDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQSKERVLLGYFDNVQFDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFPGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSIGVDYVYKAFDPRKAS 500
Db 441 SAGVSQDNLFPGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSIGVDYVYKAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG 560
Qy 561 TDGSFKGWLKYGTVGWRNKTTDSALWPTRGYLTVGNVNAEIALPGSKLQYYSATHNQWTFPP 620
Db 561 TDGSFKGWLKYGTVGWRNKTTDSALWPTRGYLTVGNVNAEIALPGSKLQYYSATHNQWTFPP 620
Qy 621 LSKTFTLMLGGEVGIAGGYGRKTEIPEFFENFYGGGLSVRGYSGTGLGPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVGIAGGYGRKTEIPEFFENFYGGGLSVRGYSGTGLGPKVYDEYGEKIS 680
Qy 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWMDGKTYDDNSSSATGGRVQNIY 740
Db 681 YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWMDGKTYDDNSSSATGGRVQNIY 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
```


PS	Claim 22; Page 32; 39pp; English.	
XX	The present invention describes an immunogenic composition (I) comprising a Neisseria antigen and an adjuvant composition comprising an oligonucleotide comprising at least 1 CG motif. Also described is an adjuvant composition (II) comprising an oligonucleotide which comprises at least 1 CG motif and a complete Freund's adjuvant (CFA), where the oligonucleotide preferably comprises at least one phosphorothioate bond. AA92359 to AA92385 represent specifically claimed oligonucleotides of the present invention. (I) is useful for stimulating an immune response in a mammal, preferably a human, against Neisseria infection, preferably Neisseria meningitidis infection and in the manufacture of a medicament for inducing a protective immune response in a mammal. The present sequence represents the claimed Neisseria meningitidis serogroup B amino acid sequence disclosed in GB-928197.4, which is given in the present invention	
XX	Sequence 797 AA;	
SQ	Query Match 94.4%; Score 752; DB 4; Length 797; Best Local Similarity 100.0%; Pred. No. 0; Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Db	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Qy	81 GQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140	
Db	81 GQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140	
Qy	141 LGRGKLNIOITPKVTKLARNRVDIITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE 200	
Db	141 LGRGKLNIOITPKVTKLARNRVDIITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE 200	
Qy	201 GGIWTLTRSNQFNEQFAQDMKVTFYQNGVDFRIIDTDIQTNEDKTKQITKITVH 260	
Db	201 GGIWTLTRSNQFNEQFAQDMKVTFYQNGVDFRIIDTDIQTNEDKTKQITKITVH 260	
Qy	261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKYERQOMTAVLGEIQNRMGSAAYS 320	
Db	261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKYERQOMTAVLGEIQNRMGSAAYS 320	
Qy	321 EISVQPLPNAETKTVDVFLHIEPGRKTYVNEIHTGNKTRDEVVRELQRMESAPYDTS 380	
Db	321 EISVQPLPNAETKTVDVFLHIEPGRKTYVNEIHTGNKTRDEVVRELQRMESAPYDTS 380	
Qy	381 KLQSKERVLLGYFDNVQPDVAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440	
Db	381 KLQSKERVLLGYFDNVQPDVAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440	
Qy	441 SAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYVKAFDPRKAS 500	
Db	441 SAGVSQDNLFCTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYVKAFDPRKAS 500	
Qy	501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAHLTVNTYNKAPKHYADFIKKYKGTG 560	
Db	501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAHLTVNTYNKAPKHYADFIKKYKGTG 560	
Qy	561 TDGSFKGLVYKGTVGWRNKTDSALWPTGRVYLTGVNAEIALPGSKLOYYSATNQWTFPP 620	
Db	561 TDGSFKGLVYKGTVGWRNKTDSALWPTGRVYLTGVNAEIALPGSKLOYYSATNQWTFPP 620	
Qy	621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680	
Db	621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680	
Qy	681 YGGNKKANVAELLFPMPGAKADARTVRLSLPADAGSVWDGKTYDDNSSSATGGRVQNIYG 740	
Db	681 YGGNKKANVAELLFPMPGAKADARTVRLSLPADAGSVWDGKTYDDNSSSATGGRVQNIYG 740	
Qy	741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772	

Db	741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772	
RESULT 9		
AAB84746		
ID	AAB84746 standard; protein; 797 AA.	
XX	XX AAB84746;	
XX	DT 17-SEP-2001 (first entry)	
DE	Amino acid sequence of a Neisseria serogroup A protein.	
XX	Serogroup A protein; outer membrane protein; Neisserial infection;	
KW	vaccine.	
XX	OS Neisseria meningitidis.	
XX	PH Key Location/Qualifiers	
FT	Peptide 1..21	
FT	/note= "signal peptide"	
FT	Protein 22..797	
FT	/note= "mature protein"	
XX	WO200152885-A1.	
XX	PD 26-JUL-2001.	
XX	17-JAN-2001; 2001WO-1B000166.	
XX	17-JAN-2000; 2000GB-00001067.	
PR	09-MAR-2000; 2000GB-00005699.	
XX	(CHIR-) CHIRON SPA.	
XX	Pizza M, Rappuoli R, Giuliani M;	
XX	WPI; 2001-451895/48.	
DR	N-PSDB; AAH421130.	
XX	Composition for treating or preventing infection to, detecting, or for raising antibodies against Neisserial bacteria, comprises an N. meningitidis serogroup B outer membrane preparation and an immunogenic component.	
XX	Disclosure; Page 71-74; 83pp; English.	
PS	The present sequence represents a Neisseria serogroup A protein. The protein is used to produce the compositions of the invention. The specification describes a composition, comprising a Neisseria meningitidis serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in WO99/57280, WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413, WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA, TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a medicament for treating or preventing infection due to Neisserial bacteria; a diagnostic reagent for detecting the presence of Neisserial bacteria; or of antibodies raised against Neisserial bacteria; and/or a reagent which can raise antibodies against Neisserial bacteria. It may also be used as a vaccine	
XX	Sequence 797 AA;	
SQ	Query Match 94.4%; Score 752; DB 4; Length 797; Best Local Similarity 100.0%; Pred. No. 0; Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Db	21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFDDVRVETAD 80	
Qy	81 GQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSYFNQATLNOAVAGLKEEY 140	

Db	81	QQLLTIVERTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEY	140
Qy	141	LGRGKLNITQITPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE	200
Db	141	LGRGKLNITQITPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQRMSLTE	200
Qy	201	GGIWTWLTNRNQFNEQKFAQDMKVDFYQNNGVDFRILDTDIQTNEDTKTQIKITVH	260
Db	201	GGIWTWLTNRNQFNEQKFAQDMKVDFYQNNGVDFRILDTDIQTNEDTKTQIKITVH	260
Qy	261	EGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQMTAVLGEIQNRMSGAYS	320
Db	261	EGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQMTAVLGEIQNRMSGAYS	320
Qy	321	EISVQPLPNAETKTVDVFLHIETPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTS	380
Db	321	EISVQPLPNAETKTVDVFLHIETPGRKIYVNEIHITGNKTRDEVVRRELQMESAPYDTS	380
Qy	381	KLQSKERVLLGYFDNVQFPAVLACTPDKVDLNMSLTERSTGSLDLQAGWQDTGLVM	440
Db	381	KLQSKERVLLGYFDNVQFPAVLACTPDKVDLNMSLTERSTGSLDLQAGWQDTGLVM	440
Qy	441	SAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAS	500
Db	441	SAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAS	500
Qy	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG	560
Db	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG	560
Qy	561	TGGSFKGWLKYGTVGWRNKDTSALPTRGYLTGVNAEIALPGSKLOVYSATHNOTWFFP	620
Db	561	TGGSFKGWLKYGTVGWRNKDTSALPTRGYLTGVNAEIALPGSKLOVYSATHNOTWFFP	620
Qy	621	LSKFTFLMLGGEVGTAGGVRGRTKEIPPFENFYGGGLSVRGVYESGTLGPKYVDEYGEKIS	680
Db	621	LSKFTFLMLGGEVGTAGGVRGRTKEIPPFENFYGGGLSVRGVYESGTLGPKYVDEYGEKIS	680
Qy	681	YGGNKKANVSARELLPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYG	740
Db	681	YGGNKKANVSARELLPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYG	740
Qy	741	AGNTHKSTFTNELRYSAGAVTWLSPLGPMKF	772
Db	741	AGNTHKSTFTNELRYSAGAVTWLSPLGPMKF	772
RESULT 10			
ID	AAB84744 standard; protein; 797 AA.		
XX			
AC	AAB84744;		
XX			
DT	17-SEP-2001 (first entry)		
XX			
DE	Amino acid sequence of a Neisseria serogroup B protein.		
XX			
KW	Serogroup B protein; outer membrane protein; Neisseria infection;		
KW	vaccine.		
XX	Neisseria meningitidis.		
XX			
FT	Key	Location/Qualifiers	
FT	Peptide	1..21	
FT		/note= "signal peptide"	
FT	Protein	22..797	
FT		/note= "mature protein"	
XX	WO200152885-A1.		
XX			
PD	26-JUL-2001.		
XX			
PF	17-JAN-2001; 2001WO-1B000166.		

XX	17-JAN-2000; 2000GB-00001067.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							</
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QY 561 TDGSPKGLYKGTGVGWRNKTDGALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSPKGLYKGTGVGWRNKTDGALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWTFPP 620
QY 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
QY 681 YGKNKKANVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGKNKKANVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
QY 741 AGNTHKSTFTNELRYSGAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGGAVTWLSPGLPMKF 772

RESULT 11
AEB93431
ID AEB93431 standard; protein; 797 AA.
AC AEB93431;
DT 20-OCT-2005 (first entry)
XX Neisseria meningitidis group B outer membrane protein Omp85.
DE Neisseria meningitidis group B outer membrane protein Omp85.
KW protein quantitation; outer membrane protein Omp85.
OS Neisseria meningitidis serogroup B.
PN US2005176085-A1.
XX 11-AUG-2005.
XX 15-NOV-2004; 2004US-00988943.
XX 19-NOV-2003; 2003CU-00000269.
XX (BETA/) BETANCOURT N L H.
PA (DORT/) DORTA-DUQUE J F D C.
PA (PERE/) PEREZ V A B.
PA (VALD/) VALDES J G.
PA (LOPE/) LOPEZ L J G.
PA (PALO/) PALOMARES G R P.
PA (FEYT/) FEYT R P.
PA (GILF/) GIL F M A.
XX Betancourt NLH, Dorta-Duque JFD, Perez VAB, Valdes JG, Lopez LJG;
PI Palomares GRP, Feyt RP, Gil FMA;
XX WPI; 2005-596348/61.
XX
XX Identifying and quantifying proteins in complex mixtures by selectively
PT isolating peptides not containing histidine nor arginine from each
PT protein, and determining the relative concentration of proteins in
PT different samples.
XX
XX Example 2; SEQ ID NO 7; 91pp; English.
XX
XX The invention relates to a method for identifying and quantifying one or
CC more proteins in complex mixtures by selectively isolating peptides not
CC containing histidine nor arginine (NHR peptides) from each protein, and
CC determining the relative concentration of one or more proteins in
CC different samples from the ratio between the areas of estimated
CC theoretical spectra for each NHR peptide labeled with different isotopes
CC in each sample. The method comprises: (a) enzymatically or chemically
CC hydrolyzing the sample or samples of proteins; (b) chemically modifying
CC alpha and epsilon amino groups (alpha- and epsilon-NH2) of every peptide
CC obtained in step (a); (c) isolating the NHR peptides by cation exchange
CC chromatography from the mixture of peptides obtained in step (b); (d)
CC identifying proteins by mass spectrometry analysis of the NHR peptides

CC obtained in step (c); (e) differential isotopic labeling of protein
CC samples previously to step (a) or during steps (a) or (b) and immediately
CC mixing at least a portion of the samples; and (f) relative quantifying of
CC more proteins in the mixtures of step (e) from the ratio between the
CC areas of estimated theoretical spectra of the pair of NHR peptides
CC identified in step (d), as well as from the ratio between the areas of
CC the estimated theoretical spectra of fragments from the NHR peptides,
CC generated in step (d). Also described is a kit for the identification and
CC quantification of proteins in complex mixtures, which comprises the
CC method mentioned above. The method and kit are useful for identifying or
CC quantifying proteins, such as those with vaccinal, therapeutic or
CC diagnostic uses, in complex mixtures. The present sequence represents an
CC outer membrane protein Omp85, which is used in an example from the
CC present invention.
XX
XX
SQ Sequence 797 AA;
Query Match 94.4%; Score 752; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 21 ADFTIQDIRVEGLQRTPESTVFNPLPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFNPLPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDATKKNLESFGLAQSOYFNQATLNQAVAGLKEEY 140
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDATKKNLESFGLAQSOYFNQATLNQAVAGLKEEY 140
QY 141 LGRGKLNIOITPKVTKLARNRVDIDITIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
Db 141 LGRGKLNIOITPKVTKLARNRVDIDITIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
QY 201 GGIWTLWTRSNQFNEQFAQDMKVTDFYQNNGYDFRILDTDIQNEBKTKQTIKITH 260
Db 201 GGIWTLWTRSNQFNEQFAQDMKVTDFYQNNGYDFRILDTDIQNEBKTKQTIKITH 260
QY 261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPKWYEROQMTAVLGEIQNRMGSAVAYS 320
Db 261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPKWYEROQMTAVLGEIQNRMGSAVAYS 320
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAFYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAFYDTS 380
QY 381 KLQRSKERVVELLYFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQRSKERVVELLYFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
QY 441 SAGVSQDNLFPGTKSAALRASRSTKTLNGSLSFDPYFTADGVSLGVDYVYKAFDPRKAS 500
Db 441 SAGVSQDNLFPGTKSAALRASRSTKTLNGSLSFDPYFTADGVSLGVDYVYKAFDPRKAS 500
QY 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560
QY 561 TDGSPKGLYKGTGVGWRNKTDGALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSPKGLYKGTGVGWRNKTDGALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNQWTFPP 620
QY 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTEIPFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
QY 681 YGKNKKANVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGKNKKANVSAELLFPMGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
QY 741 AGNTHKSTFTNELRYSGAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGGAVTWLSPGLPMKF 772

QY 121 SQYFNQATLNQAVAGLKEEYLRGKLNQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180

61 I I K S L Y A T G F F D D V R V E T A D G Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K N L E S F G L A Q 120

Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDITIDEGKSAKITDIE 180

Db 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDITIDEGKSAKITDIE 180

Qy 181 FEGNQVSDRKLQRMSLTGEGGIWTLTRS 210

Db 181 FEGNQVSDRKLQRMSLTGEGGIWTLTRS 210

RESULT 14

AAB84745

ID AAB84745 standard; protein; 792 AA.

XX AC AAB84745;

XX XX

DT 11-SEP-2003 (revised)

DT 17-SEP-2001 (first entry)

XX Amino acid sequence of a Neisseria gonorrhoeae protein.

DE Serogroup B protein; outer membrane protein; Neisserial infection;

XX vaccine.

KW Neisseria gonorrhoeae.

OS

XX Key Location/Qualifiers

FH Peptide 1..21

FT /notes= "signal peptide"

FT Protein 22..792

FT /notes= "mature protein"

XX WO200152885-A1.

PN

XX 26-JUL-2001.

PD

XX 17-JAN-2001; 2001WO-IB000166.

PF

XX 17-JAN-2000; 2000GB-00001067.

PR

XX 09-MAR-2000; 2000GB-00005699.

XX

XX (CHIR-) CHIRON SPA.

PA

XX Pizza M, Rappuoli R, Giuliani M;

PI

XX WPI; 2001-451895/48.

DR

XX N-PSDB; AAH42129.

DR

XX Composition for treating or preventing infection to, detecting, or for

PT raising antibodies against Neisserial bacteria, comprises an N.

PT meningitidis serogroup B outer membrane preparation and an immunogenic

PT component.

XX

XX Disclosure; Page 65-67; 83pp; English.

PS

XX The present sequence represents a Neisseria gonorrhoeae protein. The

CC protein is used to produce the compositions of the invention. The

CC specification describes a composition, comprising a Neisseria

CC meningitidis serogroup B outer membrane preparation and an immunogenic

CC component. The immunogenic component is protein disclosed in WO99/57280,

CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,

CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,

CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a

CC medicament for treating or preventing infection due to Neisserial

CC bacteria; a diagnostic reagent for detecting the presence of Neisserial

CC bacteria or of antibodies raised against Neisserial bacteria; and/or a

CC reagent which can raise antibodies against Neisserial bacteria. It may

CC also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS

CC field)

XX

XX Sequence 792 AA;

Qy

Db

Query Match 26.3%; Score 210; DB 4; Length 792;

Best Local Similarity 100.0%; Pred. No. 3.8e-201; Indels 0; Gaps 0;

Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLMGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Db 1 MKLKQIASALMLMGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDITIDEGKSAKITDIE 180

Db 121 SOYFNQATLNQAVAGLKEEYLGROKLNIOITPKVTKLARNRVDITIDEGKSAKITDIE 180

Qy 181 FEGNQVSDRKLQRMSLTGEGGIWTLTRS 210

Db 181 FEGNQVSDRKLQRMSLTGEGGIWTLTRS 210

RESULT 15

ABP80499

ID ABP80499 standard; protein; 792 AA.

XX AC ABP80499;

XX XX

DT 07-MAR-2003 (first entry)

DT N. gonorrhoeae amino acid sequence SEQ ID 7528.

DE

XX Antibacterial; infection; vaccine; gene therapy.

KW

XX Neisseria gonorrhoeae.

OS

XX WO200279243-A2.

PN

XX 10-OCT-2002.

PD

XX 12-FEB-2002; 2002WO-IB002069.

PF

XX 12-FEB-2001; 2001GB-00003424.

PR

XX (CHIR-) CHIRON SPA.

PA

XX Fontana MR, Pizza M, Massignani V, Monaci E;

PI

XX WPI; 2003-058415/05.

DR

XX N-PSDB; ABZ41469.

DR

XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a

PT medicament for treating or preventing N. gonorrhoeae infection.

PT

XX Disclosure; Page 736; 815pp; English.

PS

XX The present invention relates to proteins from Neisseria gonorrhoeae.

CC Also disclosed are the nucleic acid molecules encoding the proteins and

CC antibodies that specifically bind to the proteins. The composition

CC comprising the protein, nucleic acid or antibody is useful for the

CC manufacture of a medicament for treating or preventing N. gonorrhoeae

CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid

CC molecules of the invention

XX

XX Sequence 792 AA;

Qy

Db

Qy	61	IIKS	YATG	PFDD	VR	VE	TAD	G	OLL	T	W	I	E	R	P	T	I	G	S	L	N	I	T	G	A	K	M	L	O	N	D	A	I	K	N	L	E	S	F	G	L	A	Q	120												
Db	61	IIKS	YATG	PFDD	VR	VE	TAD	G	OLL	T	W	I	E	R	P	T	I	G	S	L	N	I	T	G	A	K	M	L	O	N	D	A	I	K	N	L	E	S	F	G	L	A	Q	120												
Qy	121	SOYF	NO	AT	LN	Q	A	V	A	G	L	K	E	E	Y	L	G	R	G	K	L	N	I	Q	I	T	P	K	V	T	K	L	A	R	N	R	V	D	I	D	I	T	I	D	E	G	K	S	A	K	I	T	D	I	E	180
Db	121	SOYF	NO	AT	LN	Q	A	V	A	G	L	K	E	E	Y	L	G	R	G	K	L	N	I	Q	I	T	P	K	V	T	K	L	A	R	N	R	V	D	I	D	I	T	I	D	E	G	K	S	A	K	I	T	D	I	E	180
Qy	181	FE	GN	V	S	D	R	K	L	M	R	Q	M	S	L	T	E	G	G	I	W	T	L	T	R	S	210																													
Db	181	FE	GN	V	S	D	R	K	L	M	R	Q	M	S	L	T	E	G	G	I	W	T	L	T	R	S	210																													

Search completed: April 12, 2006, 16:19:10
Job time : 231 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 12, 2006, 16:15:32 ; Search time 235 Seconds
(without alignments)
2392.792 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MLLKQIASALMMLGSLPLAF.....LKKKPEDEIQRFQQLGTTF 797

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	2	Q30912_NEIME
2	752	94.4	797	2	Q9X31_NEIME
3	752	94.4	797	2	Q9X31_NEIME
4	210	26.3	792	2	Q5F5W8_NEIG1
5	157	19.7	792	2	P95359_NEIGO
6	13	1.6	771	2	Q7NVY6_CHRVO
7	13	1.6	786	2	Q8MH2_PSEPK
8	13	1.6	787	2	Q8H14_PSEPK
9	10	1.3	765	2	Q8XZ13_RALSO
10	10	1.3	766	2	Q5NZG7_AZOSE
11	9	1.1	328	2	Q9SMN7_ARATH
12	9	1.1	361	2	Q6L543_ORYSA
13	9	1.1	362	2	Q5PP51_ARATH
14	9	1.1	435	2	Q9LXP7_ARATH
15	9	1.1	713	2	Q9ZAB1_THETH
16	9	1.1	713	2	Q5S375_THETH
17	9	1.1	713	2	Q72J38_THETH
18	9	1.1	769	2	Q4LNA0_9BURK
19	9	1.1	769	2	Q63T20_EURPS
20	9	1.1	769	2	Q62JD2_BURMA
21	9	1.1	778	2	Q7VVC2_BORPE
22	9	1.1	778	2	Q7WA52_BORPA
23	9	1.1	778	2	Q7WJ86_BORBR
24	9	1.1	796	2	Q4KHG8_PSEF5
25	9	1.1	797	2	Q9S341_PHOLU
26	9	1.1	797	2	Q7N8N9_PHOLL
27	9	1.1	952	2	Q8COX4_MOUSE
28	9	1.0	1035	2	Q9M7J0_9ROSI
29	8	1.0	55	2	Q8MTZ8_HETGL
30	8	1.0	82	1	YIM3_BEPH1
31	8	1.0	123	2	Q97L79_CLOBAB

32	8	1.0	168	2	Q51R59_MAGGR
33	8	1.0	186	2	Q9ATW3_ZEA MAYS (m
34	8	1.0	215	2	Q52K81_ARATH
35	8	1.0	225	2	Q6B441_LEMMI
36	8	1.0	225	2	Q9ZU33_ARATH
37	8	1.0	241	2	Q8H308_ORYSA
38	8	1.0	259	2	Q4J118_ICTFU
39	8	1.0	273	2	Q5E535_VIBF1
40	8	1.0	277	2	Q87PJ6_VIBPA
41	8	1.0	287	2	Q7XM73_ORYSA
42	8	1.0	290	2	Q6FRT4_CANGA
43	8	1.0	299	2	Q8NSK6_CORGL
44	8	1.0	321	2	Q86GZ0_RHIAP
45	8	1.0	333	1	GYAR_PYRO
46	8	1.0	334	1	GYAR_PYRO
47	8	1.0	334	2	Q8MTY1_RHIAP
48	8	1.0	335	1	GYAR_PYPAB
49	8	1.0	337	2	Q9KRW5_VIBCH
50	8	1.0	341	2	Q9SE52_9FABA
51	8	1.0	356	2	Q60BQ6_METCA
52	8	1.0	396	2	Q565X4_9BACT
53	8	1.0	426	2	Q81885_ARATH
54	8	1.0	428	2	Q75JP2_DICDI
55	8	1.0	429	1	FLIK_BACSU
56	8	1.0	439	2	Q7XFL9_ORYSA
57	8	1.0	439	2	Q8S7B4_ORYSA
58	8	1.0	447	2	Q65ET9_BACLD
59	8	1.0	461	2	Q93ZN9_ARATH
60	8	1.0	474	2	Q9T200_BPPH1
61	8	1.0	529	2	Q67NE9_SYMTH
62	8	1.0	552	2	Q5BA86_EMENI
63	8	1.0	558	2	Q7XK07_ORYSA
64	8	1.0	558	2	Q7XM75_ORYSA
65	8	1.0	583	2	Q911V1_PSEAE
66	8	1.0	614	2	Q4WN21_ASPFU
67	8	1.0	709	2	Q5BK84_RAT
68	8	1.0	731	2	Q57U79_9TRYP
69	8	1.0	758	2	Q82U03_NITEU
70	8	1.0	796	2	Q604T9_METCA
71	8	1.0	825	2	Q6FCG7_ACIAD
72	8	1.0	826	2	Q8EGG7_SHEON
73	8	1.0	897	2	Q5AFB7_CANAL
74	8	1.0	903	1	MSPI1_SCHPO
75	8	1.0	948	2	Q500C2_PSESY
76	8	1.0	1024	2	Q4MXX2_BACCE
77	8	1.0	1025	2	Q4VIM8_BACCE
78	8	1.0	1055	2	Q57XC5_9TRYP
79	8	1.0	1066	2	Q6NP12_DROME
80	8	1.0	1085	2	Q8FQNO_COREF
81	8	1.0	1107	2	Q5BDB6_EMENI
82	8	1.0	1286	2	Q5ARD3_EMENI
83	8	1.0	1353	2	Q5AS15_EMENI
84	8	1.0	1363	1	ILPR_BRALA
85	8	1.0	1459	2	Q75G47_ORYSA
86	8	1.0	1475	2	Q9LOU6_ARATH
87	8	1.0	1548	2	Q4SUI6_TETNG
88	8	1.0	1577	1	HLVA_PROMI
89	8	1.0	2408	2	Q9V549_DROME
90	8	1.0	2903	2	Q4GZ26_9TRYP
91	8	1.0	4919	2	Q9ZHL0_HAEDU
92	8	1.0	6199	2	Q6JANO_BRARE
93	7	0.9	37	2	Q4XRS3_PLACH
94	7	0.9	53	2	Q4X6P2_PIACH
95	7	0.9	62	2	Q4K8A2_PSEF5
96	7	0.9	63	2	Q8TE37_HUMAN
97	7	0.9	65	2	Q8ZUE9_NITEU
98	7	0.9	67	2	Q8TMO2_STRCL
99	7	0.9	71	2	Q8XM23_CLOPE
100	7	0.9	75	2	Q83LQ3_SHIFL
101	7	0.9	75	2	Q8X5D6_ECO57
102	7	0.9	76	1	DICC_ECOLI
103	7	0.9	85	2	Q4NKU1_9M1CC
104	7	0.9	85	2	Q6DOU7_ERWCT

Q51R59	magnaporthe
Q9ATW3	zea mayds (m
Q52K81	arabidopsis
Q6B441	lemna minor
Q9ZU33	arabidopsis
Q8H308	oryza sativ
Q4J118	icalalurus p
Q5E535	vibrio fisc
Q87PJ6	vibrio para
Q7XM73	oryza sativ
Q6FRT4	candida gla
Q8NSK6	corynebacte
Q86GZ0	rhipecephal
Q5JE22	pyrococcus
Q58320	pyrococcus
Q8MTY1	rhipecephal
Q9UYR1	pyrococcus
Q9KRW5	vibrio chol
Q9SE52	eriosema ps
Q60BQ6	methyllococc
Q565X4	uncultured
Q81885	arabidopsis
Q75JR2	dictyosteli
P23451	bacillus su
Q7XFL9	oryza sativ
Q8S7B4	oryza sativ
Q65ET9	bacillus li
Q93ZN9	arabidopsis
Q9T200	bacterioph
Q67NE9	symbiobacte
Q5BA86	aspergillus
Q7XK07	oryza sativ
Q7XM75	oryza sativ
Q911V1	pseudomonas
Q4WN21	aspergillus
Q5BK84	rattus norv
Q57U79	trypanosoma
Q82U03	nitrosomona
Q604T9	methyllococc
Q6FCG7	acinetobact
Q8EGG7	shewanella
Q5AFB7	candida alb
P87320	schizosacch
Q500C2	pseudomonas
Q4MXX2	bacillus ce
Q4VIM8	bacillus ce
Q57XC5	trypanosoma
Q6NP12	drosophila
Q8FGN0	corynebacte
Q5BDB6	aspergillus
Q5ARD3	aspergillus
Q5AS15	aspergillus
Q02466	branchiosco
Q75G47	oryza sativ
Q91QU6	arabidopsis
Q4SUI6	tetraodon n
P16466	proteus mir
Q9V549	drosophila
Q4GZ26	trypanosoma
Q9ZHL0	haemophilus
Q6JANO	brachydanio
Q4XRS3	plasmodium
Q4X6P2	plasmodium
Q4K8A2	pseudomonas
Q8CE37	homo sapien
Q8ZUE9	nitrosomona
Q8TMO2	streptomyce
Q8XM23	clostridium
Q83LQ3	shigella fl
Q8X5D6	escherichia
P06965	escherichia
Q4NKU1	arthrobacte
Q6DOU7	erwinia car

105	7	0.9	89	2	Q5GT8_WOLTR	Q5gte8 wolbachia s
106	7	0.9	92	2	Q4KA61_PSEFS	Q4ka61 pseudomonas
107	7	0.9	93	2	Q726R5_DESVH	Q726r5 desulfovibr
108	7	0.9	95	2	Q9XXG0_CAEEL	Q9xxg0 caenorhabdi
109	7	0.9	98	2	Q6G599_BARHE	Q6g599 bartonella
110	7	0.9	101	1	PHS_STRCO	Q6g722 streptomyc
111	7	0.9	101	2	Q76445_CAEEL	Q76445 caenorhabdi
112	7	0.9	102	1	RL21_METKA	Q8tuu3 methanopyru
113	7	0.9	104	2	Q9IN54_9VIRU	Q9in54 citrus psor
114	7	0.9	104	2	Q9IN56_9VIRU	Q9in56 citrus psor
115	7	0.9	104	2	Q9IN57_9VIRU	Q9in57 citrus psor
116	7	0.9	104	2	Q9IN58_9VIRU	Q9in58 citrus psor
117	7	0.9	104	2	Q9IN59_9VIRU	Q9in59 citrus psor
118	7	0.9	104	2	Q9IN60_9VIRU	Q9in60 citrus psor
119	7	0.9	109	2	Q9Y9U5_AERPE	Q9y9u5 aeropyrum p
120	7	0.9	109	2	Q4SBE1_TETNG	Q4sbel tetraodon n
121	7	0.9	113	2	Q5OU24_IDILO	Q5qu24 idiomarina
122	7	0.9	115	2	Q7S7S3_NEUCR	Q7s7s3 neurospora
123	7	0.9	115	2	Q8RSN6_9BACT	Q8rsn6 uncultured
124	7	0.9	118	2	Q59TAI_CANAL	Q59tai candida alb
125	7	0.9	120	2	Q6COL2_KLUJA	Q6col2 kluyveromyc
126	7	0.9	123	1	KNG_GADMO	P83856 gadus morhu
127	7	0.9	123	2	Q7QBV1_ANOGA	Q7qbv1 anopheles g
128	7	0.9	124	1	CRCB_PHOLL	Q7n768 photorhabdu
129	7	0.9	125	2	Q4ZT38_PSESY	Q4zt38 pseudomonas
130	7	0.9	126	2	Q9VW79_DROME	Q9vw79 drosophila
131	7	0.9	127	2	Q06096_METWP	Q06096 methanococ
132	7	0.9	128	2	Q9C266_NEUCR	Q9c266 neurospora
133	7	0.9	130	2	Q9PV14_9PERC	Q9pv14 mola mola (
134	7	0.9	130	2	Q76CV7_CONMY	Q76cv7 conger myri
135	7	0.9	131	2	Q93773_9ARCH	Q93773 uncultured
136	7	0.9	131	2	Q9A7L3_CAUCR	Q9a7l3 caulobacter
137	7	0.9	133	2	Q58LE7_9CAUD	Q58le7 cyanophage
138	7	0.9	133	2	Q5ENK0_HETTR	Q5enk0 heterocapsa
139	7	0.9	134	2	Q8PN27_XANAC	Q8pn27 xanthomonas
140	7	0.9	135	2	Q45783_CAEEL	Q45783 caenorhabdi
141	7	0.9	138	2	Q7X116_9BACT	Q7x116 leptospiril
142	7	0.9	139	2	Q7RZL4_NEUCR	Q7rzl4 neurospora
143	7	0.9	140	2	Q9EMS9_AMEPV	Q9ems9 amsacta moo
144	7	0.9	143	2	Q5GUV4_XANOR	Q5guv4 xanthomonas
145	7	0.9	145	2	Q5KW12_GEOKA	Q5kw12 geobacillus
146	7	0.9	145	2	Q91110_WORSA	Q91110 worone saxa
147	7	0.9	148	2	Q50574_BACPF	Q50574 bacillus ps
148	7	0.9	150	1	SSRP_CAMJE	Q9pni9 campylobact
149	7	0.9	150	1	SSRP_CAMJR	Q5htz9 campylobact
150	7	0.9	150	2	Q4HG9P_CAMCO	Q4hgp9 campylobact
151	7	0.9	150	2	Q6D5B1_ERWCT	Q6d5b1 erwinia car
152	7	0.9	151	2	Q5LA18_BACFN	Q5la18 bacteroides
153	7	0.9	154	2	Q4HEM1_9DEIO	Q4hml1 deinococcus
154	7	0.9	156	2	Q70T64_CIOIN	Q70t64 ciona intes
155	7	0.9	157	2	Q8ETJ7_OCEIH	Q8etj7 oceanobacil
156	7	0.9	163	2	Q8GY17_ARATH	Q8gy17 arabidopsis
157	7	0.9	164	2	Q7R6G1_GIALA	Q7r6g1 giardia lam
158	7	0.9	165	2	Q6EPF5_ORYSA	Q6epf5 oryza sativ
159	7	0.9	168	2	Q9DKM2_9VIRU	Q9dkm2 spodoptera
160	7	0.9	169	1	YLZ6_CAEEL	P34419 caenorhabdi
161	7	0.9	169	2	Q60YR5_CAEBR	Q60yr5 caenorhabdi
162	7	0.9	170	2	Q5MQH4_9BRAD	Q5mqh4 bradyrhizob
163	7	0.9	170	2	Q5MQG6_9BRAD	Q5mqg6 bradyrhizob
164	7	0.9	170	2	Q5MQQ0_9BRAD	Q5mqq0 bradyrhizob
165	7	0.9	170	2	Q5MQF3_9BRAD	Q5mqf3 bradyrhizob
166	7	0.9	170	2	Q5MQF0_9BRAD	Q5mqf0 bradyrhizob
167	7	0.9	170	2	Q5MQB7_9BRAD	Q5mqb7 bradyrhizob
168	7	0.9	170	2	Q5MQB4_9BRAD	Q5mqe4 bradyrhizob
169	7	0.9	170	2	Q5MQB3_9BRAD	Q5mqe3 bradyrhizob
170	7	0.9	170	2	Q5MQB2_9BRAD	Q5mqe2 bradyrhizob
171	7	0.9	170	2	Q5MQB0_9BRAD	Q5mqe0 bradyrhizob
172	7	0.9	170	2	Q5MQB8_9BRAD	Q5mqe8 bradyrhizob
173	7	0.9	170	2	Q5MQH2_9BRAD	Q5mqh2 bradyrhizob
174	7	0.9	170	2	Q5MQD8_9BRAD	Q5mqd8 bradyrhizob
175	7	0.9	170	2	Q5MQB5_BRAEL	Q5mqe5 bradyrhizob
176	7	0.9	170	2	Q5MQG3_9BRAD	Q5mqg3 bradyrhizob
177	7	0.9	170	2	Q5MQF1_BRAJA	Q5mqf1 bradyrhizob

178	7	0.9	170	2	Q5MQF9_BRAJA	Q5mqf9 bradyrhizob
179	7	0.9	170	2	Q5MQF6_BRAJA	Q5mqf6 bradyrhizob
180	7	0.9	171	2	Q9ZAL7_LISIV	Q9zal7 listeria iv
181	7	0.9	171	2	Q97QH7_STRPN	Q97qh7 streptococ
182	7	0.9	172	2	Q9JGT9_9RHAB	Q9jgt9 northern ce
183	7	0.9	175	2	Q4WDX4_9SPFU	Q4wdx4 aspergillus
184	7	0.9	175	2	Q9SVE4_ARATH	Q9sve4 arabidopsis
185	7	0.9	176	2	Q8SRN5_ENCCU	Q8srn5 encephalito
186	7	0.9	177	2	Q676Z8_9ASPA	Q676z8 hyacinthus
187	7	0.9	177	2	Q9R8W8_9RHIZ	Q9r8w8 rhizobium s
188	7	0.9	177	2	Q9R8X0_9RHIZ	Q9r8x0 rhizobium s
189	7	0.9	177	2	Q9R8X1_9RHIZ	Q9r8x1 rhizobium s
190	7	0.9	177	2	Q9R8X2_9RHIZ	Q9r8x2 rhizobium s
191	7	0.9	177	2	Q9Z3N0_9RHIZ	Q9z3n0 rhizobium s
192	7	0.9	177	2	Q5WF12_9BRAD	Q5wfp12 bradyrhizob
193	7	0.9	177	2	Q5WF10_9BRAD	Q5wfp10 bradyrhizob
194	7	0.9	177	2	Q5WP09_9BRAD	Q5wp09 bradyrhizob
195	7	0.9	177	2	Q5WP08_9BRAD	Q5wp08 bradyrhizob
196	7	0.9	177	2	Q5WP07_9BRAD	Q5wp07 bradyrhizob
197	7	0.9	177	2	Q5WP06_9BRAD	Q5wp06 bradyrhizob
198	7	0.9	178	2	Q9Z3N4_9RHIZ	Q9z3n4 rhizobium s
199	7	0.9	179	2	Q6H0X9_9CREN	Q6h0x9 sulfolobus
200	7	0.9	180	2	Q84IV2_MYCLE	Q84iv2 mycobacteri
201	7	0.9	184	2	Q26429_METTH	Q26429 methanobact
202	7	0.9	184	2	Q6NE26_9VIRU	Q6ne26 leptospira
203	7	0.9	184	2	Q6FCT9_ACTAD	Q6fct9 acinetobact
204	7	0.9	185	2	Q63WA2_BURPS	Q63wa2 burkholderi
205	7	0.9	185	2	Q62LF2_BURMA	Q62lf2 burkholderi
206	7	0.9	187	2	Q83NG0_TROW8	Q83ng0 tropheryma
207	7	0.9	189	2	Q4RR79_TETNG	Q4rr79 tetraodon n
208	7	0.9	190	2	Q782U6_9ALPH	Q782u6 gallid herp
209	7	0.9	190	2	Q9QTE3_9ALPH	Q9qte3 marek's dis
210	7	0.9	193	2	Q8VUA8_9LACT	Q8vua8 lactococcus
211	7	0.9	194	2	Q6CY36_KLUJA	Q6cy36 kluyveromyc
212	7	0.9	194	2	Q7XYA3_GRIJA	Q7xya3 griffithsia
213	7	0.9	196	2	Q8LMY9_ORYSA	Q8lmy9 oryza sativ
214	7	0.9	196	2	Q7THD4_9PICO	Q7thd4 aichi virus
215	7	0.9	196	2	Q7THD5_9PICO	Q7thd5 aichi virus
216	7	0.9	196	2	Q7THD6_9PICO	Q7thd6 aichi virus
217	7	0.9	197	2	Q4FPR2_9RICK	Q4fpr2 candidatus
218	7	0.9	197	2	Q83N11_TROWT	Q83n11 tropheryma
219	7	0.9	199	2	Q62M56_BURMA	Q62m56 burkholderi
220	7	0.9	202	1	HIS7_RHIME	Q92tb0 rhizobium m
221	7	0.9	205	2	Q6CVD5_KLUJA	Q6cvd5 kluyveromyc
222	7	0.9	207	1	THIE_CHRVO	Q7plr3 chromobacte
223	7	0.9	207	2	Q7PXH3_ANOGA	Q7pxh3 anopheles g
224	7	0.9	210	2	Q5WID5_BACSG	Q5wid5 bacillus cl
225	7	0.9	212	2	Q5EJ95_LACAC	Q5fj95 lactobacill
226	7	0.9	214	1	NODB_RHIGA	Q503s4 rhizobium g
227	7	0.9	214	2	Q627B7_CAEBR	Q627b7 caenorhabdi
228	7	0.9	214	2	Q9CD65_MYCLE	Q9cd65 mycobacteri
229	7	0.9	216	2	Q6FXH5_CANGA	Q6fxh5 candida gla
230	7	0.9	216	2	Q7NFC9_GLOVI	Q7nfc9 gloeobacter
231	7	0.9	218	2	Q9Z5F9_MYCLE	Q9z5f9 mycobacteri
232	7	0.9	218	2	Q63YC9_BURPS	Q63yc9 burkholderi
233	7	0.9	218	2	Q6E2U7_BURMA	Q6e2u7 burkholderi
234	7	0.9	221	2	Q8KK26_PROVU	Q8kk26 proteus vul
235	7	0.9	221	2	Q6D4J2_ERWCT	Q6d4j2 erwinia car
236	7	0.9	223	1	KCY_NITEU	Q82td5 nitrosomona
237	7	0.9	223	2	Q4TNP6_9SPHN	Q4tnp6 erythrobact
238	7	0.9	225	2	Q8KT67_PHOLU	Q8kt67 photorhabdu
239	7	0.9	225	2	Q7N025_PHOUL	Q7n025 photorhabdu
240	7	0.9	226	2	Q9VLK7_DROME	Q9vlk7 drosophila
241	7	0.9	226	2	Q96SW3_CAEEL	Q96sw3 caenorhabdi
242	7	0.9	227	2	Q63S36_BURPS	Q63s36 burkholderi
243	7	0.9	227	2	Q5Q2P8_IDILO	Q5q2p8 idiomarina
244	7	0.9	228	2	Q9EMK6_AMEPV	Q9emk6 amsacta moo
245	7	0.9	230	2	Q7QBH1_ANOGA	Q7qbh1 anopheles g
246	7	0.9	231	2	Q4VMH3_9EURO	Q4vmh3 neosartoria
247	7	0.9	231	2	Q4VMH5_9EURO	Q4vmh5 neosartoria
248	7	0.9	231	2	Q53LL3_ORYSA	Q53ll3 oryza sativ
249	7	0.9	231	2	Q4K719_PSEFS	Q4k719 pseudomonas
250	7	0.9	231	2	Q5LWA8_SILPO	Q5lwa8 silicibacte

251	7	0.9	233	2	Q9RJPL_STRCO	Q9rjpl streptomyc	324	7	0.9	288	2	Q8W190_EUGR	Q8w190 euglena gra
252	7	0.9	233	2	Q7U5M9_SYNXP	Q7u5m9 synchococ	325	7	0.9	288	2	Q823B6_CHLCV	Q823b6 chlamydophi
253	7	0.9	234	2	Q25327_HELPJ	Q25327 hellobacte	326	7	0.9	289	2	Q743L1_MYCPA	Q743l1 mycobacteri
254	7	0.9	234	2	Q9ZLM6_HELPJ	Q9zlm6 hellobacte	327	7	0.9	290	2	Q749V5_GEOSL	Q749v5 geobacter s
255	7	0.9	235	2	Q7NWX8_CHRNO	Q7nwx8 chromobacte	328	7	0.9	291	2	Q615Z1_CAENR	Q615z1 caenorhabdi
256	7	0.9	238	2	Q7XBL0_9MAGN	Q7xbl0 pachysandra	329	7	0.9	291	2	Q30441_BORFE	Q30441 bordetella
257	7	0.9	238	2	Q4ZU73_PSESY	Q4zu73 pseudomonas	330	7	0.9	291	2	Q7W3M9_BORPA	Q7w3m9 bordetella
258	7	0.9	238	2	Q8HYM6_PSEAE	Q8hym6 pseudomonas	331	7	0.9	291	2	Q7W3M9_BORPA	Q7w3m9 bordetella
259	7	0.9	238	2	Q822R1_PSESM	Q822r1 pseudomonas	332	7	0.9	292	2	Q7W3M9_BORPA	Q7w3m9 bordetella
260	7	0.9	241	2	Q68961_HELPY	Q68961 hellobacte	333	7	0.9	292	2	Q9REA4_ENTFA	Q9rea4 enterococcu
261	7	0.9	242	2	Q5J161_PYRKO	Q5j161 pyrococcus	334	7	0.9	292	2	Q5TRH6_ANOGA	Q5trh6 anopheles g
262	7	0.9	242	2	Q6GMW5_9MAGN	Q6gmw5 akedia trif	335	7	0.9	295	2	Q9ERF5_MESAU	Q9erf5 mesocricetu
263	7	0.9	242	2	Q7U774_SYNXP	Q7u774 synchococ	336	7	0.9	296	2	Q4IQE4_GIBZE	Q4iqe4 gibberella
264	7	0.9	243	2	Q7N9U3_PHOLL	Q7n9u3 photorhabdu	337	7	0.9	297	2	Q7SG71_NEUCR	Q7sg71 neurospora
265	7	0.9	243	2	Q89DF6_BRAJA	Q89df6 bradyrhizob	338	7	0.9	297	2	Q5B0V7_EMENI	Q5b0v7 aspergillus
266	7	0.9	246	2	Q601LO_MYCHA	Q601lo mycoplasma	339	7	0.9	298	2	Q9GL74_CERAE	Q9gl74 cercopithe
267	7	0.9	246	2	Q98FG4_RHILO	Q98fg4 rhizobium l	340	7	0.9	298	2	Q9M9T0_WOLSU	Q9m9t0 wolinnella s
268	7	0.9	246	2	Q8PUT8_METMA	Q8put8 methanosarc	341	7	0.9	299	2	Q7QPM1_GIALA	Q7qpm1 giardia lam
269	7	0.9	248	2	Q98K42_RHILO	Q98k42 rhizobium l	342	7	0.9	299	2	Q8D4T3_VIBVU	Q8d4t3 vibrio vuln
270	7	0.9	248	2	Q8TJK1_METAC	Q8tjk1 methanosarc	343	7	0.9	299	2	Q7MGD6_VIBVU	Q7mgd6 vibrio vuln
271	7	0.9	249	2	Q8LAW6_BACCR	Q8law6 bacillus ce	344	7	0.9	301	2	Q8PXU9_METMA	Q8pxu9 methanosarc
272	7	0.9	254	2	Q7SAF5_NEUCR	Q7saf5 neurospora	345	7	0.9	301	2	Q82B65_STRAW	Q82b65 streptomyc
273	7	0.9	254	2	Q946T1_SORBI	Q946t1 sorghum bic	346	7	0.9	304	2	Q8FRS6_COREF	Q8frs6 corynebacte
274	7	0.9	255	2	Q8CY97_STRR6	Q8cy97 streptococ	347	7	0.9	305	2	Q9RT24_DEIRA	Q9rt24 deinfotale
275	7	0.9	255	2	Q97NR2_STRPN	Q97nr2 streptococ	348	7	0.9	305	2	Q6APE9_DESPS	Q6ape9 desulfotale
276	7	0.9	255	2	Q5FRW9_GLUOX	Q5frw9 gluconobact	349	7	0.9	306	2	Q7RUI7_NEUCR	Q7rui7 neurospora
277	7	0.9	256	2	Q4K6W1_PSEFF5	Q4k6w1 pseudomonas	350	7	0.9	306	2	Q8UCH5_AGRTS	Q8uch5 agrobacteri
278	7	0.9	257	1	HADD_RHISH	Q8k1s9 rhizobium s	351	7	0.9	306	2	Q61W15_CAEBR	Q61w15 caenorhabdi
279	7	0.9	259	2	Q5YTX5_NOCFA	Q5ytx5 nocardia fa	352	7	0.9	307	2	Q61W15_CAEBR	Q61w15 caenorhabdi
280	7	0.9	260	2	Q87ST1_VIBPA	Q87st1 vibrio para	353	7	0.9	307	2	Q8LCAZ_ARATH	Q8lcaz arabidopsis
281	7	0.9	264	2	Q4ILN6_GIBZE	Q4iln6 gibberella	354	7	0.9	308	2	Q84L58_CICAR	Q84l58 cicier ariet
282	7	0.9	264	2	Q8NSS7_DROME	Q8nes7 drosophila	355	7	0.9	308	2	Q8FCP5_ECOL6	Q8fcp5 escherichia
283	7	0.9	264	2	Q5L6W4_CHLAB	Q5l6w4 chlamydophi	356	7	0.9	308	2	Q828C9_STRJK	Q828c9 streptomyc
284	7	0.9	264	2	Q84478_CHLTR	Q84478 chlamydia t	357	7	0.9	311	2	Q4JUC2_CORJK	Q4juc2 corynebacte
285	7	0.9	264	2	Q5YPD0_NOCFA	Q5ypd0 nocardia fa	358	7	0.9	311	2	Q8U9T2_AGRTS	Q8u9t2 agrobacteri
286	7	0.9	264	2	Q824J5_CHLCV	Q824j5 chlamydophi	359	7	0.9	312	2	Q60KQ8_CAEBR	Q60kq8 caenorhabdi
287	7	0.9	264	2	Q9P1S1_CHLMU	Q9p1s1 chlamydia m	360	7	0.9	312	2	Q5FS46_GLUOX	Q5fs46 gluconobact
288	7	0.9	265	2	Q4FUC8_9GNMM	Q4fuc8 psychrobact	361	7	0.9	313	2	Q4NV47_9DELT	Q4nv47 anaeromyxob
289	7	0.9	266	2	Q5LSY3_CHLAB	Q5lsy3 chlamydophi	362	7	0.9	314	2	Q8LPG2_ARATH	Q8lpg2 arabidopsis
290	7	0.9	266	2	Q8CES7_MOUSE	Q8ces7 mus musculu	363	7	0.9	315	2	Q55K19_CRYNE	Q55k19 cryptococcu
291	7	0.9	267	2	Q6I1I3_DROME	Q6i1i3 drosophila	364	7	0.9	315	2	Q5KAY2_CRYNE	Q5kay2 cryptococcu
292	7	0.9	267	2	Q893R1_CLOTE	Q893r1 clostridium	365	7	0.9	315	2	Q9FVX5_ARATH	Q9fvx5 arabidopsis
293	7	0.9	267	2	Q7AC45_GEOSL	Q7ac45 geobacter s	366	7	0.9	316	2	Q82W49_NITEU	Q82w49 nitrosomona
294	7	0.9	267	2	Q7NGC3_GLOVI	Q7ngc2 thermoplasm	367	7	0.9	316	2	Q65566_9ALPH	Q65566 bovine herp
295	7	0.9	268	1	AROK_THEAC	Q7ngc5 streptomyc	368	7	0.9	316	2	Q77CC0_9ALPH	Q77cc0 corynebacte
296	7	0.9	268	2	Q86780_STRCO	Q86780 streptomyc	369	7	0.9	317	2	Q7N4V6_PHOLL	Q7n4v6 photorhabdu
297	7	0.9	269	2	Q81IU2_PLAF7	Q81iu2 plasmodium	370	7	0.9	317	2	Q6N9N0_RHOPA	Q6n9n0 rhodospseudo
298	7	0.9	269	2	Q9XAC7_STRCO	Q9xac7 streptomyc	371	7	0.9	320	1	FLAA1_TREHY	FLAA1 treponema h
299	7	0.9	270	2	Q6BT18_DEBHA	Q6bt18 debaryomyce	372	7	0.9	320	2	Q6H4W3_ORYSA	Q6h4w3 oryza sativ
300	7	0.9	272	2	Q5LI12_BACFN	Q5li12 bacteroides	373	7	0.9	322	2	Q57SJ2_SALCH	Q57sj2 salmonella
301	7	0.9	272	2	Q64ZK6_BACFR	Q64zk6 bacteroides	374	7	0.9	324	2	Q5PFX0_SALPA	Q5pfx0 salmonella
302	7	0.9	273	2	Q620W7_ORYSA	Q620w7 oryza sativ	375	7	0.9	324	2	Q7CR48_SALTY	Q7cr48 salmonella
303	7	0.9	274	2	Q50VM4_ENTHI	Q50vm4 entamoeba h	376	7	0.9	324	2	Q8XGHO_SALTI	Q8xgho salmonella
304	7	0.9	274	2	Q41VD6_AZOVI	Q41vd6 azotobacter	377	7	0.9	325	2	Q9P753_NEUCR	Q9p753 neurospora
305	7	0.9	274	2	Q87KK2_VIBPA	Q87kk2 vibrio para	378	7	0.9	325	2	Q9FAA4_9CORY	Q9faa4 brevivibact
306	7	0.9	277	2	Q4PHA7_USTMA	Q4pha7 ustilago ma	379	7	0.9	325	2	Q4KJ77_PSEF5	Q4kjt7 pseudomonas
307	7	0.9	277	2	Q7YZT2_TRYCO	Q7yzt2 trypanosoma	380	7	0.9	325	2	Q79VG6_CORGL	Q79vg6 corynebacte
308	7	0.9	277	2	Q5WP13_9BRAD	Q5wp13 bradyrhizob	381	7	0.9	325	2	Q6NHT0_CORDI	Q6nht0 corynebacte
309	7	0.9	277	2	Q5WP11_9BRAD	Q5wp11 bradyrhizob	382	7	0.9	326	2	Q8FQ21_COREF	Q8fq21 corynebacte
310	7	0.9	278	2	Q4WNH5_ASPFU	Q4wnh5 aspergillus	383	7	0.9	326	2	Q5RKJ0_RAT	Q5rkj0 rattus norv
311	7	0.9	279	2	Q758X7_ASHGO	Q758x7 ashbya gos	384	7	0.9	326	2	Q6NQC3_ARATH	Q6nqc3 arabidopsis
312	7	0.9	279	2	Q6F3A1_MOUSE	Q6p3a1 mus musculu	385	7	0.9	328	2	Q9RB11_PSCCC	Q9rb11 pectobacter
313	7	0.9	280	1	CBIO1_STRF3	Q59vy7 streptococ	386	7	0.9	328	2	Q9B111_RHOBA	Q9b111 rhodopirell
314	7	0.9	280	1	CBIO1_STRF6	Q59yb6 streptococ	387	7	0.9	329	2	Q7USN3_CANAL	Q7usn3 candida alb
315	7	0.9	280	1	CBIO1_STRP8	Q7cmm8 streptococ	388	7	0.9	329	2	Q4JVK6_CORJK	Q4jvk6 corynebacte
316	7	0.9	280	1	CBIO1_STRPV	Q99x12 streptococ	389	7	0.9	330	2	Q4RBI1_TETNG	Q4rb11 tetraodon n
317	7	0.9	280	2	Q5UYN3_HALMA	Q5uy3 haloarcula	390	7	0.9	330	2	Q5N78_CANAL	Q5n78 candida alb
318	7	0.9	280	2	P90872_CAEBL	P90872 caenorhabdi	391	7	0.9	331	2	Q7U9S8_SYNXP	Q7u9s8 synchococ
319	7	0.9	280	2	Q9ABA2_CAUCR	Q9a8a2 caulobacter	392	7	0.9	331	2	Q71118_9HIV1	Q71118 human immun
320	7	0.9	281	2	Q8DUM0_STRMU	Q8dum0 streptococ	393	7	0.9	332	2	Q5ATH3_EMENI	Q5ath3 aspergillus
321	7	0.9	282	2	Q96NE7_HUMAN	Q96ne7 homo sapien	394	7	0.9	332	2	Q5N2U1_SYNPE	Q5n2u1 synchococ
322	7	0.9	283	2	Q9RJF9_STRCO	Q9rjf9 streptomyc	395	7	0.9	333	2	Q4I337_GIBZE	Q4i337 gibberella
323	7	0.9	287	1	PSA3_YEAST	P21242 saccharomyc	396	7	0.9				

397	7	0.9	333	2	Q88VL6_LACPL	Q88VL6 lactobacill	470	7	0.9	360	2	Q5JP96_HUMAN	Q5JP96 homo sapien
398	7	0.9	335	2	Q92PW3_ARATH	Q92PW3 arabidopsis	471	7	0.9	360	2	Q54MCS_DICDI	Q54MCS dictyosteli
399	7	0.9	335	2	Q71115_9HIV1	Q71115 human immun	472	7	0.9	360	2	Q8D7X9_VIBVU	Q8D7X9 vibrio vuln
400	7	0.9	335	2	Q71116_9HIV1	Q71116 human immun	473	7	0.9	360	2	Q7MEZ5_VIBVY	Q7MEZ5 vibrio vuln
401	7	0.9	335	2	Q71117_9HIV1	Q71117 human immun	474	7	0.9	361	2	Q6L1J2_PICTO	Q6L1J2 picrophilus
402	7	0.9	335	2	Q71120_9HIV1	Q71120 human immun	475	7	0.9	361	2	Q82WK0_NITEU	Q82WK0 nitrosomona
403	7	0.9	335	2	Q71320_9HIV1	Q71320 human immun	476	7	0.9	362	1	LDOX_VITVI	P51031 vitis vinif
404	7	0.9	336	1	QKNKI_MOUSE	Q8581 mus musculus	477	7	0.9	362	1	RECA_BRAJA	Q89184 bradyrhizob
405	7	0.9	336	1	OTCC_STRP3	P65609 streptococc	478	7	0.9	362	2	Q8T114_PHYPO	Q8T114 physarum po
406	7	0.9	336	1	OTCC_STRP6	Q5XV4 streptococc	479	7	0.9	362	2	Q73V31_MYCPA	Q73V31 mycobacteri
407	7	0.9	336	1	OTCC_STRP8	P65610 streptococc	480	7	0.9	362	2	Q6GN23_XENLA	Q6GN23 xenopus lae
408	7	0.9	336	1	OTCC_STRPY	P16964 streptococc	481	7	0.9	363	1	LEU3A_ASPNG	P87256 aspergillus
409	7	0.9	336	1	Q99L39_MOUSE	Q99L39 mus musculus	482	7	0.9	363	2	Q60MN7_CASBR	Q60MN7 caenorhabdi
410	7	0.9	337	1	GIMA2_HUMAN	Q9UG22 homo sapien	483	7	0.9	364	2	Q877A9_ASPOR	Q877A9 aspergillus
411	7	0.9	337	1	OTCC2_STRA3	P65605 streptococc	484	7	0.9	364	2	Q52GH3_MAGGR	Q52GH3 magnaporthe
412	7	0.9	337	1	OTCC2_STRA5	P65606 streptococc	485	7	0.9	366	2	Q5BEW8_EMENI	Q5BEW8 aspergillus
413	7	0.9	337	1	OTCC_STRAG	Q8RP83 streptococc	486	7	0.9	366	2	Q4WRM6_ASPFU	Q4WRM6 aspergillus
414	7	0.9	337	1	Q5RCT2_PONPY	Q5RC12 pongo pygma	487	7	0.9	367	2	Q60B60_METCA	Q60B60 methylococc
415	7	0.9	337	2	Q4RP53_TETNG	Q4RP53 tetraodon n	488	7	0.9	367	2	Q98G12_RHILO	Q98G12 rhizobium l
416	7	0.9	339	2	Q4WEN6_ASPFU	Q4WEN6 aspergillus	489	7	0.9	369	2	Q5YM04_ORYSA	Q5YM04 o hypotheti
417	7	0.9	339	2	Q5DMW2_ARATH	Q5DMW2 arabidopsis	490	7	0.9	369	2	Q5Z4G5_ORYSA	Q5Z4G5 oryza sativ
418	7	0.9	339	2	Q8C9Y2_MOUSE	Q8C9Y2 mus musculus	491	7	0.9	369	2	Q5Z4H4_ORYSA	Q5Z4H4 oryza sativ
419	7	0.9	340	2	Q9G644_9SAUR	Q9G644 calotes cal	492	7	0.9	369	2	Q7ZWM8_XENLA	Q7ZWM8 xenopus lae
420	7	0.9	341	2	Q5KMW9_GEOKA	Q5KMW9 geobacillus	493	7	0.9	370	2	Q4Q7Z3_LEIMA	Q4Q7Z3 leishmania
421	7	0.9	341	2	Q98CD7_RHILO	Q98CD7 rhizobium l	494	7	0.9	370	2	Q27855_TETHH	Q27855 tetrahymena
422	7	0.9	341	2	Q7UJ82_RHOBA	Q7UJ82 rhodopirell	495	7	0.9	371	2	Q73RV5_MYCPA	Q73RV5 mycobacteri
423	7	0.9	342	1	OST6_HUMAN	Q96Q15 homo sapien	496	7	0.9	371	2	Q8FR78_COREF	Q8FR78 corynebacte
424	7	0.9	342	1	Q5H9K7_HUMAN	Q5H9K7 homo sapien	497	7	0.9	371	2	Q6R796_9HERP	Q6R796 oreitrid her
425	7	0.9	343	1	Q5YV31_NOCFA	Q5YV31 nocardia fa	498	7	0.9	373	1	SECU_YEAST	P40316 saccharomyc
426	7	0.9	344	1	RNF2_XENLA	Q66J69 xenopus lae	499	7	0.9	374	2	Q4XX42_PLACH	Q4XX42 plasmodium
427	7	0.9	344	2	Q4WXG1_ASPFU	Q4WXG1 aspergillus	500	7	0.9	375	1	RECA_RHOBA	Q7UJ10 rhodopirell
428	7	0.9	344	2	Q4XG06_ACTPL	Q4XG06 actinobacil	501	7	0.9	375	2	Q708E2_9CAUD	Q708E2 bactariopha
429	7	0.9	344	2	Q4IYW1_AZOVI	Q4IYW1 azotobacter	502	7	0.9	376	2	Q76L01_9CILU	Q76L01 dileptus ma
430	7	0.9	344	2	Q630X0_BACCZ	Q630X0 bacillus ce	503	7	0.9	376	2	Q7WZC5_LACJO	Q7WZC5 lactobacill
431	7	0.9	345	2	Q6P164_HUMAN	Q6P164 homo sapien	504	7	0.9	377	1	RING1_CANFA	Q5TJF3 canis famil
432	7	0.9	346	1	ETFL_CRYNE	Q8I0W1 cryptococcu	505	7	0.9	377	1	RING1_HUMAN	Q06597 homo sapien
433	7	0.9	346	1	Q5DAI8_SCHJA	Q5DAI8 schistosoma	506	7	0.9	377	1	RING1_MACMU	Q8WMN5 macaca mula
434	7	0.9	346	2	Q3REP7_PONPY	Q3REP7 pongo pygma	507	7	0.9	377	2	Q35730_MOUSE	Q35730 mus musculu
435	7	0.9	347	2	Q9SU74_ARATH	Q9SU74 arabidopsis	508	7	0.9	377	2	Q6MGB6_RAT	Q6MGB6 rattus norv
436	7	0.9	347	2	Q8SH97_BROPE	Q8SH97 brookesia p	509	7	0.9	377	2	Q921I28_MOUSE	Q921I28 mus musculu
437	7	0.9	347	2	Q8SH43_BROBR	Q8SH43 brookesia b	510	7	0.9	377	2	Q4FK33_MOUSE	Q4FK33 mus musculu
438	7	0.9	348	2	Q52EH4_MAGGR	Q52EH4 magnaporthe	511	7	0.9	377	2	Q8AV27_CHICK	Q8AV27 gallus gall
439	7	0.9	348	2	Q8REG8_9NOCA	Q8REG8 rhodococcus	512	7	0.9	379	2	Q57G04_BRUAB	Q57G04 bruceella ab
440	7	0.9	348	2	Q70PA6_9DELT	Q70PA6 mellitangiu	513	7	0.9	379	2	Q8G3E1_BRUSU	Q8G3E1 bruceella su
441	7	0.9	348	2	Q5LBF9_BACFN	Q5LBF9 bacteroides	514	7	0.9	380	2	Q9KYW7_STRCO	Q9KYW7 streptomyce
442	7	0.9	348	2	Q64R21_BACFR	Q64R21 bacteroides	515	7	0.9	380	2	Q8YEE1_BRUME	Q8YEE1 bruceella me
443	7	0.9	349	1	ISPG_CLOAB	Q97I56 clostridium	516	7	0.9	381	2	Q4UEB8_THEAN	Q4UEB8 theileria a
444	7	0.9	349	2	Q51A59_ENTHI	Q51A59 entamoeba h	517	7	0.9	382	2	Q5P656_AZOSE	Q5P656 azoarcus sp
445	7	0.9	349	2	Q8CF87_MOUSE	Q8CF87 mus musculu	518	7	0.9	382	2	Q7MT14_PORGI	Q7MT14 porphyromon
446	7	0.9	351	2	Q66K46_HUMAN	Q66K46 homo sapien	519	7	0.9	382	2	Q5YXR8_9NOCA	Q5YXR8 nocardia fa
447	7	0.9	351	2	Q70AX1_ACTTI	Q70AX1 actinoplane	520	7	0.9	382	2	Q6NWD4_BRARE	Q6NWD4 brachydanio
448	7	0.9	351	2	Q6AL26_DESPS	Q6AL26 desulfofale	521	7	0.9	383	2	Q8KWF1_BACST	Q8KWF1 bacillus st
449	7	0.9	351	2	Q6NS95_MOUSE	Q6NS95 mus musculu	522	7	0.9	383	2	Q6UD24_9PROT	Q6UD24 uncultured
450	7	0.9	352	2	Q5BCG1_EMENI	Q5BCG1 aspergillus	523	7	0.9	383	2	Q6UD50_9PROT	Q6UD50 uncultured
451	7	0.9	353	2	Q4R617_WACPA	Q4R617 macaca fasc	524	7	0.9	383	2	Q63IN7_BURPS	Q63IN7 burkholderi
452	7	0.9	353	2	Q5Z2G5_ACTTI	Q5Z2G5 actinoplane	525	7	0.9	383	2	Q8NR26_CORGL	Q8NR26 corynebacte
453	7	0.9	353	2	Q5YT17_NOCFA	Q5YT17 nocardia fa	526	7	0.9	384	2	Q9FSQ3_ORYSA	Q9FSQ3 oryza sativ
454	7	0.9	354	2	Q99XC6_STAAN	Q99XC6 staphylococ	527	7	0.9	384	2	Q40492_TOBAC	Q40492 nicotiana t
455	7	0.9	355	1	PHBC_CHRVI	P45370 c poly-beta	528	7	0.9	384	2	Q921J4_RHIME	Q921J4 rhizobium m
456	7	0.9	355	2	Q9C778_ARATH	Q9C778 arabidopsis	529	7	0.9	385	2	Q8TR21_METAC	Q8TR21 methanosaar
457	7	0.9	355	2	Q4W0V9_ARATH	Q4W0V9 arabidopsis	530	7	0.9	385	2	Q5YXD4_9NOCA	Q5YXD4 nocardia fa
458	7	0.9	355	2	Q31252_9NOST	Q31252 anaebena sp	531	7	0.9	386	2	Q7VS16_EORFE	Q7VS16 bordetella
459	7	0.9	355	2	Q6GD41_STAAS	Q6GD41 staphylococ	532	7	0.9	386	2	Q7WEB8_BORBR	Q7WEB8 bordetella
460	7	0.9	355	2	Q5HJT9_STAAC	Q5HJT9 staphylococ	533	7	0.9	387	1	RECA_LEFBI	P48290 leptospira
461	7	0.9	355	2	Q7NK07_GLOVI	Q7NK07 gloeobacter	534	7	0.9	387	2	Q6PFK0_BRARE	Q6PFK0 brachydanio
462	7	0.9	355	2	Q8NVY5_STAAM	Q8NVY5 staphylococ	535	7	0.9	388	1	XYLA_STRCK	Q96324 streptomyce
463	7	0.9	355	2	Q8YV41_ANASP	Q8YV41 anaebena sp	536	7	0.9	388	2	Q4NLG9_9MICC	Q4NLG9 arthrobacte
464	7	0.9	357	2	Q7NZ0J_CHRVO	Q7NZ0J chromobacte	537	7	0.9	390	2	Q8PV83_METNA	Q8PV83 methanosaar
465	7	0.9	358	1	RECA_MYXXA	P48292 myxococcus	538	7	0.9	390	2	Q9LIV7_ARATH	Q9LIV7 arabidopsis
466	7	0.9	358	2	Q4Q699_LEIMA	Q4Q699 leishmania	539	7	0.9	390	2	Q4NE55_9MICC	Q4NE55 arthrobacte
467	7	0.9	358	2	Q4NPR7_9DELT	Q4NPR7 anaeromyxob	540	7	0.9	390	2	Q5WHZ3_BACSK	Q5WHZ3 bacillus cl
468	7	0.9	358	2	Q81PE1_BACAN	Q81PE1 bacillus an	541	7	0.9	391	2	Q8T3J1_DROME	Q8T3J1 drosophila
469	7	0.9	358	2	Q7SZ55_BRARE	Q7SZ55 brachydanio	542	7	0.9	392	2	Q4YS02_PLABE	Q4YS02 plasmodium

543	7	0.9	392	2	Q4MHB9_BACCE	Q4mhb9 bacillus ce	616	7	0.9	428	2	Q747R9_GEOSL	Q747r9 geobacter s
544	7	0.9	393	2	Q7RST8_PLAYO	Q7rst8 plasmodium	617	7	0.9	429	1	SYS_PHOLL	Q7nce7 photorhabdu
545	7	0.9	393	2	Q5KV50_GEOKA	Q5kv50 geobacillus	618	7	0.9	429	2	Q8VCL3_BRUME	Q8vcl3 bruceella me
546	7	0.9	393	2	Q65F04_BACLD	Q65f04 bacillus l1	619	7	0.9	430	2	Q7RAW2_PLAYO	Q7raw2 plasmodium
547	7	0.9	394	2	Q8IK92_PLAF7	Q8ik92 plasmodium	620	7	0.9	431	2	Q21194_CABEL	Q21194 caenorhabdi
548	7	0.9	394	2	Q9R672_SYNP6	Q9r672 synechococc	621	7	0.9	431	2	Q8HT85_9TRAC	Q8ht85 selaginella
549	7	0.9	394	2	Q6HXK4_BACAN	Q6hxx4 bacillus an	622	7	0.9	431	2	Q7JM29_TREDE	Q7jrm29 treponema d
550	7	0.9	394	2	Q5LVC8_SILPO	Q5lvc8 silicibacte	623	7	0.9	431	2	Q66H32_RAT	Q66h32 rattus norv
551	7	0.9	397	2	Q4HZ87_GIBZE	Q4hz87 gibberella	624	7	0.9	432	2	Q5AZG5_EMENI	Q5azg5 aspergillus
552	7	0.9	397	2	Q5DWM4_ARATH	Q5dwm4 arabidopsis	625	7	0.9	432	2	Q4KCI5_PSEF5	Q4kci5 pseudomonas
553	7	0.9	398	2	Q89E17_BRAJA	Q89e17 bradyrhizob	626	7	0.9	432	2	Q6NWF0_BRARE	Q6nwf0 brachydanio
554	7	0.9	399	1	ENO_ARCFU	Q29133 archaeoglob	627	7	0.9	434	2	Q5ASG9_EMENI	Q5asg9 aspergillus
555	7	0.9	401	2	Q5B621_EMENI	Q5b621 aspergillus	628	7	0.9	434	2	Q9TXJ4_LEIMA	Q9txj4 leishmania
556	7	0.9	401	2	Q911P8_PSEAE	Q911p8 pseudomonas	629	7	0.9	435	2	Q6G2S5_BARHE	Q6g2s5 bartonella
557	7	0.9	402	2	Q9FLE1_LACAC	Q9fle1 lactobacill	630	7	0.9	435	2	Q836C0_ENTFA	Q836c0 enterococcu
558	7	0.9	402	2	Q8ET06_OCEIH	Q8et06 oceanobacil	631	7	0.9	436	2	Q4K3C1_PSEF5	Q4k3c1 pseudomonas
559	7	0.9	404	2	Q6BG17_PARTE	Q6bg17 paramecium	632	7	0.9	437	2	Q6D2L6_ERWCT	Q6d2l6 erwinia car
560	7	0.9	404	2	Q6SH30_9BACT	Q6sh30 uncultured	633	7	0.9	437	2	Q7NHM7_GLOVI	Q7nhm7 gloeobacter
561	7	0.9	405	2	Q9NV04_HUMAN	Q9nv04 homo sapien	634	7	0.9	438	2	Q6BCG8_EDWIC	Q6bcg8 edwardsiell
562	7	0.9	406	2	Q86V19_HUMAN	Q86v19 homo sapien	635	7	0.9	439	2	Q4ROX6_TETNG	Q4rox6 tetraodon n
563	7	0.9	406	2	Q5TJF4_CANFA	Q5tj4 canis famil	636	7	0.9	439	2	Q4Q698_LEIMA	Q4q698 leishmania
564	7	0.9	406	2	Q4KMC1_RAT	Q4kmc1 rattus norv	637	7	0.9	440	2	Q4TAU6_TETNG	Q4ta6 tetraodon n
565	7	0.9	407	2	Q5PXG6_SPOSC	Q5pxg6 sporothrix	638	7	0.9	441	2	Q4WCZ8_ASPFU	Q4wc28 aspergillus
566	7	0.9	407	2	Q6YPR8_ORYSA	Q6yp8 oryza sativ	639	7	0.9	442	2	Q5GUF1_XANOR	Q5guf1 xanthomonas
567	7	0.9	408	2	Q6CMJ5_KIULA	Q6cmj5 kluyveromyc	640	7	0.9	442	2	Q5NTF9_9BACT	Q5ntf9 uncultured
568	7	0.9	409	1	PRX12_PICPA	Q01961 pichia past	641	7	0.9	443	2	Q23497_CABEL	Q23497 caenorhabdi
569	7	0.9	410	2	Q51L21_MAGGR	Q51l21 magnapothre	642	7	0.9	444	2	Q89M95_BRAJA	Q89m95 bradyrhizob
570	7	0.9	410	2	Q51F48_ENTHI	Q51f48 entamoeba h	643	7	0.9	444	2	Q89NW0_BRAJA	Q89nw0 bradyrhizob
571	7	0.9	410	2	Q4Q1S8_LEIMA	Q4q1s8 leishmania	644	7	0.9	445	2	Q4HRF7_CAMUP	Q4hrf7 campylobact
572	7	0.9	410	2	Q8E2R6_STR3	Q8e2r6 streptococc	645	7	0.9	445	2	Q6N715_RHOPA	Q6n715 rhodospseudo
573	7	0.9	410	2	Q6AB18_PROAC	Q6ab18 propionibac	646	7	0.9	446	2	Q7SB26_NEUCR	Q7sb26 neurospora
574	7	0.9	411	2	Q5NPX0_ZYMMO	Q5npx0 zymononas m	647	7	0.9	446	2	Q6BU59_DEBHA	Q6bus9 debaryomyce
575	7	0.9	412	2	Q580B2_9TRYP	Q580b2 trypanosoma m	648	7	0.9	448	2	Q5J361_PYRKO	Q5j361 pyrococcus
576	7	0.9	412	2	Q9Z5T5_ZYMMO	Q9z5t5 zymononas m	649	7	0.9	451	1	Q8Y1V0_BALSO	Q8y1v0 kalsstonia s
577	7	0.9	412	2	Q41V81_AZOV1	Q41v81 azotobacter	650	7	0.9	451	1	VPS9_YEAST	Q34787 saccharomyc
578	7	0.9	413	2	Q961Z5_HUMAN	Q961z5 homo sapien	651	7	0.9	453	2	Q6A855_PROAC	Q6a855 propionibac
579	7	0.9	413	2	Q5J5N8_HUMAN	Q5j5n8 homo sapien	652	7	0.9	453	2	Q5A418_CANAL	Q5a418 candida alb
580	7	0.9	413	2	Q8E7Q7_VIBF1	Q8e7q7 vibrio fisc	653	7	0.9	455	2	Q57794_PYROCO	Q57794 pyrococcus
581	7	0.9	413	2	Q8JZV4_MOUSE	Q8jzv4 m riken cdm	654	7	0.9	456	2	Q7QB46_ANOGA	Q7qb46 anopheles g
582	7	0.9	414	1	CDC61_METAC	Q8tur2 methanosarc	655	7	0.9	456	2	Q8R9H8_THETN	Q8r9h8 thermoplaea
583	7	0.9	414	1	CDC61_METMA	Q5jet2 pyrococcus	656	7	0.9	459	2	Q881M9_PSESM	Q881m9 pseudomonas
584	7	0.9	415	1	CDC6_PYRKO	Q5757q0 ashbya goss	657	7	0.9	460	2	Q98RZ3_GUITH	Q98rz3 guillardia
585	7	0.9	415	1	PGK_ASHGO	Q6guc8 staphylococ	658	7	0.9	460	2	Q74GQ7_GEOSL	Q74gq7 geobacter s
586	7	0.9	416	2	Q6GCU8_STAAS	Q6guc8 staphylococ	659	7	0.9	461	2	Q6JKE9_9NUCL	Q6jke9 neodiprion
587	7	0.9	416	2	Q6GKCB_STAAR	Q6gkc8 staphylococ	660	7	0.9	462	2	Q57ZN8_9TRYP	Q57zn8 trypanosoma
588	7	0.9	416	2	Q5HJ05_STAAC	Q5hj05 staphylococ	661	7	0.9	463	2	Q41LH4_GIBZE	Q41lh4 gibberella
589	7	0.9	416	2	Q7A1Y3_STAAN	Q7a1y3 staphylococ	662	7	0.9	463	2	Q6SY98_PHOLU	Q6sy98 photorhabdu
590	7	0.9	416	2	Q7A814_STAAN	Q7a814 staphylococ	663	7	0.9	464	2	Q7Z3Y7_HUMAN	Q7z3y7 homo sapien
591	7	0.9	416	2	Q99X43_STAAM	Q99x43 staphylococ	664	7	0.9	466	2	Q5DBX8_SCHJA	Q5dbx8 schistosoma
592	7	0.9	417	1	PGK_CANMA	P41757 candida mal	665	7	0.9	466	2	Q579C6_BRUAB	Q579c6 bruceella ab
593	7	0.9	418	2	Q41FL6_GIBZE	Q41fl6 gibberella	666	7	0.9	466	2	Q8FVD7_BRUSU	Q8fvd7 deinoococcus
594	7	0.9	418	2	Q8DWM5_STRAS	Q8dwm5 streptococc	667	7	0.9	467	2	Q4H6R7_9DEIO	Q4h6r7 halobacteri
595	7	0.9	419	1	CDC6_PYRAB	Q9v2f2 pyrococcus	668	7	0.9	469	2	Q51997_HALISA	Q51997 halobacteri
596	7	0.9	419	1	CDC6_PYRHO	Q57864 pyrococcus	669	7	0.9	469	2	Q6CSM6_KIULA	Q6csm6 kluyveromyc
597	7	0.9	419	1	YAML_RHISN	P55571 rhizobium s	670	7	0.9	469	2	Q41BZ4_GIBZE	Q41bz4 gibberella
598	7	0.9	419	2	Q4WBZ3_ASPFU	Q4wbz3 aspergillus	671	7	0.9	469	2	Q6AF02_LEIXX	Q6af02 leifsonia x
599	7	0.9	420	1	CDC6_PYRFU	P81413 pyrococcus	672	7	0.9	471	2	Q9E2F8_9TRYP	Q9e2f8 streptococc
600	7	0.9	420	1	Y1541_METJA	Q58936 methanococc	673	7	0.9	471	2	Q9E2F8_9TRYP	Q9e2f8 streptococc
601	7	0.9	420	1	Q9RJQ6_STRCO	Q9rjq6 streptomyc	674	7	0.9	471	2	Q92CE1_LISIN	Q92ce1 listeria in
602	7	0.9	421	2	Q5TPJ5_ANOGA	Q5tpj5 anopheles g	675	7	0.9	472	2	Q9F2B6_THAAR	Q9f2b6 thauera aro
603	7	0.9	421	2	Q9SV69_TETTH	Q9sv69 tetrahymena	676	7	0.9	472	2	Q9F2B6_THAAR	Q9f2b6 thauera aro
604	7	0.9	422	1	LACE_AGRD	P29822 agrobacteri	677	7	0.9	473	1	DNAA_PORGI	Q7mx21 porphyromon
605	7	0.9	422	1	Q5BHU6_DROME	Q5bhu6 drosophila	678	7	0.9	473	2	Q71211_STRTE	Q71211 streptomyc
606	7	0.9	422	2	Q57LY9_SALCH	Q57ly9 salmonella	679	7	0.9	473	2	Q84142_9ACTO	Q84142 streptomyc
607	7	0.9	422	2	Q5PCV3_SALPA	Q5pcv3 salmonella	680	7	0.9	475	2	Q6Y636_MOUSE	Q6y636 mus musculu
608	7	0.9	422	2	Q82NC0_SALTY	Q8nc0 salmonella	681	7	0.9	476	2	Q41695_GIBZE	Q41695 gibberella
609	7	0.9	423	2	Q5RBZ5_PONPY	Q5rbz5 pongo pygma	682	7	0.9	476	2	Q8U552_AGR5	Q8u552 agrobacteri
610	7	0.9	423	2	Q93256_CHICK	Q93256 gallus gall	683	7	0.9	477	2	Q7V9V6_PROMA	Q7v9v6 prochloroco
611	7	0.9	424	2	Q89R42_BRAJA	Q89r42 bradyrhizob	684	7	0.9	477	2	Q87HT2_VIBPA	Q87ht2 vibrio para
612	7	0.9	424	2	Q4HL64_CAMLA	Q4hl64 campylobact	685	7	0.9	478	2	Q8S8J0_TETNG	Q8s8j0 tetraodon n
613	7	0.9	427	2	Q60947_TRYCR	Q60947 trypanosoma	686	7	0.9	480	2	Q6R2R8_9VIRU	Q6r2r8 hyposoter d
614	7	0.9	428	2	Q5R891_PONPY	Q5r891 pongo pygma	687	7	0.9	481	2	Q7Q2A3_ANOGA	Q7q2a3 anopheles g
615	7	0.9	428	2	P74349_SYNY3	P74349 synechocyst	688	7	0.9	482	2	Q892C7_CLOTE	Q892c7 clostridium

589	7	0.9	483	2	Q531B6_STRGR	Q531b6 streptomyc	762	7	0.9	546	2	Q7UT65_RHOBA	Q7ut65 rhodopi
590	7	0.9	485	2	Q4Q263_LEIMA	Q4q263 leishmania	763	7	0.9	547	2	Q7SAW8_ASHGO	Q7SAW8 ashbya
591	7	0.9	485	2	Q6WU7_RHIZOB	Q6WU7 rhizobium	764	7	0.9	547	2	Q8AJJ6_BACTN	Q8AJJ6 bacteroides
592	7	0.9	485	2	Q731L4_TREDE	Q731L4 treponema	765	7	0.9	547	2	Q7J378_TREDE	Q7J378 treponema
593	7	0.9	486	2	Q62P84_HUMAN	Q62P84 homo sapien	766	7	0.9	549	2	Q4NU97_9DELT	Q4NU97 anaeromyxob
594	7	0.9	487	2	Q8U0H5_PYRTU	Q8U0H5 pyrococcus	767	7	0.9	549	2	Q4NUZ1_9DELT	Q4NUZ1 anaeromyxob
595	7	0.9	487	2	Q578Q5_BRUAB	Q578Q5 brucella	768	7	0.9	550	2	Q9RB11_ACIAA	Q9RB11 acinetobact
596	7	0.9	487	2	Q7SXF3_BRARE	Q7SXF3 brachydanio	769	7	0.9	550	2	Q6FCC3_ACIAA	Q6FCC3 acinetobact
597	7	0.9	488	2	Q6PJJ6_HUMAN	Q6PJJ6 homo sapien	770	7	0.9	551	2	Q6JUV5_MAIZE	Q6JUV5 zea mays
598	7	0.9	488	2	Q524G6_ORYSA	Q524G6 oryza sativ	771	7	0.9	556	2	Q5B706_EMENI	Q5B706 aspergillus
599	7	0.9	488	2	Q528M4_ORYSA	Q528M4 oryza sativ	772	7	0.9	556	2	Q810A1_MOUSE	Q810A1 mus musculus
700	7	0.9	488	2	Q8S1B1_ORYSA	Q8S1B1 oryza sativ	773	7	0.9	556	2	Q9D972_MOUSE	Q9D972 mus musculus
701	7	0.9	488	2	Q5YM05_ORYSA	Q5YM05 o. hypotheti	774	7	0.9	562	1	CH60_TREYR	Q95046 trypanosoma
702	7	0.9	488	2	Q89H76_BRAJA	Q89H76 bradyrhizob	775	7	0.9	562	2	Q8NK91_ASFOR	Q8NK91 aspergillus
703	7	0.9	489	1	CP128_MYCBO	CP128 mycobacteri	776	7	0.9	562	2	Q7SAY9_ASHGO	Q7SAY9 ashbya
704	7	0.9	489	1	CP128_MYCTU	CP128 mycobacteri	777	7	0.9	562	2	Q9V725_DROME	Q9V725 drosophila
705	7	0.9	489	1	OCNL_POTTR	OCNL potorous tr	778	7	0.9	562	2	Q4Q1M0_LEIMA	Q4Q1M0 leishmania
706	7	0.9	490	2	Q54WV0_DICDI	Q54WV0 dictyosteli	779	7	0.9	564	2	Q9PQT6_UREPA	Q9PQT6 ureaplasma
707	7	0.9	491	2	Q5LYN0_STR11	Q5LYN0 streptococc	780	7	0.9	567	2	Q9HGH9_ASFOR	Q9HGH9 aspergillus
708	7	0.9	491	2	Q5M393_STR12	Q5M393 streptococc	781	7	0.9	568	2	Q59WU0_CANAL	Q59WU0 candida
709	7	0.9	493	2	Q761Y0_ORYSA	Q761Y0 oryza sativ	782	7	0.9	568	2	Q524M2_MAGGR	Q524M2 magnaporthe
710	7	0.9	497	2	Q8DQ91_STR16	Q8DQ91 streptococc	783	7	0.9	572	2	Q6ZH86_ORYSA	Q6ZH86 oryza sativ
711	7	0.9	497	2	Q97RD6_STRPN	Q97RD6 streptococc	784	7	0.9	573	2	Q9VDS0_DROME	Q9VDS0 drosophila
712	7	0.9	498	2	Q97V40_SULSO	Q97V40 sulfolobus	785	7	0.9	575	2	Q6S1P7_BACLD	Q6S1P7 bacillus
713	7	0.9	498	2	Q6X195_9CAUD	Q6X195 bacterioph	786	7	0.9	578	2	Q5GH49_FUGRU	Q5GH49 fugu rubrip
714	7	0.9	499	2	Q6X1A1_9CAUD	Q6X1A1 bacterioph	787	7	0.9	579	2	Q5BD66_EMENI	Q5BD66 aspergillus
715	7	0.9	500	2	Q6X1A2_BPR03	Q6X1A2 bacterioph	788	7	0.9	580	2	Q89YL8_BACTN	Q89YL8 bacteroides
716	7	0.9	501	2	Q6X1A3_BPT6	Q6X1A3 bacterioph	789	7	0.9	581	2	Q6T807_9PAST	Q6T807 manheimia
717	7	0.9	502	1	DNAA_MYCLE	DNAA mycobacteri	790	7	0.9	583	1	ARSA2_ECOLI	P52145 escherichia
718	7	0.9	502	2	Q5Q3F0_9CAUD	Q5Q3F0 enterobacte	791	7	0.9	583	1	ARSA2_ECOLI	P52145 escherichia
719	7	0.9	503	2	Q8MQF7_CABEL	Q8MQF7 caenorhabdi	792	7	0.9	583	2	Q798A6_9ZZZZ	Q798A6 inen plaemi
720	7	0.9	503	2	Q8EK00_SHEON	Q8EK00 shewanella	793	7	0.9	584	2	Q9NNT7_RHILX	Q9NNT7 rhizobium
721	7	0.9	505	2	Q5WNC5_CABER	Q5WNC5 caenorhabdi	794	7	0.9	585	2	Q9KJ13_KLEBO	Q9KJ13 klebsiella
722	7	0.9	506	2	Q17537_CABEL	Q17537 caenorhabdi	795	7	0.9	586	2	Q59FG5_HUMAN	Q59FG5 homo sapien
723	7	0.9	507	2	Q6CB84_YARLI	Q6CB84 yarrowia	796	7	0.9	587	1	RGPI_HUMAN	P46060 homo sapien
724	7	0.9	508	2	P90790_CABEL	P90790 caenorhabdi	797	7	0.9	588	2	Q6L1L2_PICTO	Q6L1L2 picophilus
725	7	0.9	508	2	Q9VBP7_DROME	Q9VBP7 drosophila	798	7	0.9	589	1	RGPI_MOUSE	P46061 mus musculus
726	7	0.9	509	2	Q8D0L7_YERPE	Q8D0L7 yerinia	799	7	0.9	589	2	Q53M56_ORYSA	Q53M56 oryza sativ
727	7	0.9	510	2	Q7QKE9_ANOGA	Q7QKE9 anopheles	800	7	0.9	589	2	Q91YS2_MOUSE	Q91YS2 mus musculus
728	7	0.9	510	2	Q5FUI9_GLUOX	Q5FUI9 gluconobact	801	7	0.9	589	2	Q8C2E3_MOUSE	Q8C2E3 mus musculus
729	7	0.9	512	2	Q5AQP6_EMENI	Q5AQP6 aspergillus	802	7	0.9	589	2	Q7TWM1_MOUSE	Q7TWM1 mus musculus
730	7	0.9	514	2	Q9DF59_BRARE	Q9DF59 brachydanio	803	7	0.9	589	2	Q6NZB5_MOUSE	Q6NZB5 mus musculus
731	7	0.9	515	1	PVRI_MOUSE	Q9JK6 mus musculus	804	7	0.9	590	2	Q5FL18_LACAC	Q5FL18 lactobacill
732	7	0.9	515	1	PVRI_PIG	Q9G176 sus scrofa	805	7	0.9	592	2	Q5R4P2_PONPY	Q5R4P2 pongo pygma
733	7	0.9	515	2	Q97Y93_SULSO	Q97Y93 sulfolobus	806	7	0.9	594	2	Q8GJK0_DICDI	Q8GJK0 dictyosteli
734	7	0.9	516	2	Q6P9M9_MOUSE	Q6P9M9 mus musculus	807	7	0.9	596	2	Q6X194_9CAUD	Q6X194 bacterioph
735	7	0.9	516	2	Q7MQB5_VIBVY	Q7MQB5 vibrio vuln	808	7	0.9	596	2	Q6X197_BPR32	Q6X197 bacterioph
736	7	0.9	517	1	PVRI_HUMAN	Q15223 homo sapien	809	7	0.9	596	2	Q6X198_BPR27	Q6X198 bacterioph
737	7	0.9	518	1	CDC63_HALSA	Q9HMS3 halobacteri	810	7	0.9	596	2	Q6X199_9CAUD	Q6X199 bacterioph
738	7	0.9	518	2	Q747N5_GEOSL	Q747N5 geobacter	811	7	0.9	596	2	Q6X1A0_9CAUD	Q6X1A0 bacterioph
739	7	0.9	519	2	Q7S8P0_NEUCR	Q7S8P0 neurospora	812	7	0.9	596	2	Q6X1A4_9CAUD	Q6X1A4 bacterioph
740	7	0.9	524	1	CDC64_HALMA	Q5U224 haloarcula	813	7	0.9	596	2	Q6T811_9PAST	Q6T811 manheimia
741	7	0.9	524	2	Q5CE67_CRYHO	Q5CE67 cryptospori	814	7	0.9	596	2	Q4S436_TETNG	Q4S436 tetraodon
742	7	0.9	526	1	KIC10_BOVIN	P06394 bos taurus	815	7	0.9	597	2	Q4PA83_USTMA	Q4PA83 ustilago
743	7	0.9	526	2	Q8RMB3_ALCEU	Q8RMB3 alcaligenes	816	7	0.9	603	2	Q5L5D2_CHLAB	Q5L5D2 chlamydomo
744	7	0.9	527	2	Q4LSI3_9BURK	Q4LSI3 burkholderi	817	7	0.9	603	2	Q5FQZ2_GLOOX	Q5FQZ2 gluconobact
745	7	0.9	527	2	Q63A80_BACCZ	Q63A80 bacillus ce	818	7	0.9	604	2	Q04098_ARATH	Q04098 arabidopsis
746	7	0.9	527	2	Q6HMM4_BACHK	Q6HMM4 bacillus th	819	7	0.9	605	1	NRDD_BPT4	P07071 bacterioph
747	7	0.9	529	2	Q9FDI3_9MICO	Q9FDI3 revibacter	820	7	0.9	605	2	Q6BP07_DEBHA	Q6BP07 debaryomyce
748	7	0.9	532	2	Q7NYE6_CHRVO	Q7NYE6 chromobacte	821	7	0.9	605	2	Q7V558_BPR69	Q7V558 bacterioph
749	7	0.9	536	2	Q4P008_USTMA	Q4P008 ustilago ma	822	7	0.9	610	2	Q8W6J7_9CAUD	Q8W6J7 einorhizobi
750	7	0.9	537	1	YDU2_SCHPO	Q6MD44 parachlamyd	823	7	0.9	610	2	Q63ST4_BURPS	Q63ST4 burkholderi
751	7	0.9	537	1	YDU2_SCHPO	Q13863 schizosacch	824	7	0.9	610	2	Q62J44_BURMA	Q62J44 burkholderi
752	7	0.9	537	2	Q8Q934_9CORA	Q8Q934 avian infec	825	7	0.9	612	2	Q91ZF4_9LUTE	Q91ZF4 cereal yell
753	7	0.9	541	2	Q4W0D6_ASPFU	Q4W0D6 aspergillus	826	7	0.9	614	2	Q4M0L8_9BURK	Q4M0L8 burkholderi
754	7	0.9	541	2	Q5B014_EMENI	Q5B014 aspergillus	827	7	0.9	616	1	GLMS_AERPE	Q9YCG6 a glucosami
755	7	0.9	543	2	Q6D418_ERWCT	Q6D418 erwinia car	828	7	0.9	617	2	Q5YU10_NOCFA	Q5YU10 nocardia
756	7	0.9	545	2	Q7QY12_GIALA	Q7QY12 giardia lam	829	7	0.9	619	1	CALX_CAEEL	Q34652 caenorhabdi
757	7	0.9	545	2	Q6NJCS_CORDI	Q6NJCS corynebacte	830	7	0.9	620	1	ORC2_YEAST	P32833 saccharomyc
758	7	0.9	545	2	Q8ZE13_YERPE	Q8ZE13 yerinia	831	7	0.9	622	2	Q5ZIM1_CHICK	Q5ZIM1 gallus gall
759	7	0.9	545	2	Q66A41_YERPS	Q66A41 yerinia	832	7	0.9	623	2	Q96J72_HUMAN	Q96J72 homo sapien
760	7	0.9	546	2	Q5E722_VIBFI	Q5E722 vibrio fisc	833	7	0.9	623	2	Q61J15_CABER	Q61J15 caenorhabdi
761	7	0.9	546	2	Q4NZX2_9DELT	Q4NZX2 anaeromyxob	834	7	0.9	623	2	Q8YQB8_ANASP	Q8YQB8 anabaena

835	7	0.9	626	2	Q55N18_BACLD	Q65n18 bacillus li	908	2	Q6FSW0_CANGA	Q6fsw0 candida gla
836	7	0.9	628	2	Q82H05_STRAW	Q82hq5 streptomyce	909	2	Q5H419_XANOR	Q5h419 xanthomonas
837	7	0.9	631	2	Q51XM6_MAGGR	Q5ixm6 magnaporthe	910	2	Q5H6E3_XANOR	Q5h6e3 xanthomonas
838	7	0.9	632	1	HIP14_HUMAN	Q8iuh5 homo sapien	911	2	Q9H2G6_HUMAN	Q9h2g6 homo sapien
839	7	0.9	632	1	HIP14_HUMAN	Q80tn5 mus musculus	912	2	Q9H2G6_HUMAN	Q9h2g6 bacteroides
840	7	0.9	632	1	HIP14_HUMAN	Q7u778 synechococc	913	2	Q55BF3_DICDI	Q55bf3 dictyosteli
841	7	0.9	632	2	Q5DMW3_ARATH	Q5dmw3 arabidopsis	914	2	Q55BF3_DICDI	Q55bf3 dictyosteli
842	7	0.9	634	2	Q4PAL6_USTMA	Q4paz6 ustilago ma	915	2	Q55BF3_DICDI	Q55bf3 dictyosteli
843	7	0.9	641	2	Q9KWU1_9SPHN	Q9kwu1 spingomonas	916	2	Q55BF3_DICDI	Q55bf3 dictyosteli
844	7	0.9	645	2	Q5NT68_THITH	Q5nt68 thibacillu	917	2	Q55BF3_DICDI	Q55bf3 dictyosteli
845	7	0.9	646	2	Q6ZPH4_MOUSE	Q6zph4 mus musculus	918	2	Q55BF3_DICDI	Q55bf3 dictyosteli
846	7	0.9	647	2	Q73NK7_TREDE	Q73nk7 treponema d	919	2	Q55BF3_DICDI	Q55bf3 dictyosteli
847	7	0.9	649	1	LONH_METJA	Q58812 methanococc	920	2	Q55BF3_DICDI	Q55bf3 dictyosteli
848	7	0.9	649	2	Q4PIEL_USTMA	Q4piel ustilago ma	921	2	Q55BF3_DICDI	Q55bf3 dictyosteli
849	7	0.9	651	2	Q6TKP9_HUMAN	Q6tkp9 homo sapien	922	2	Q55BF3_DICDI	Q55bf3 dictyosteli
850	7	0.9	651	2	Q4Q848_LEIMA	Q4q848 leishmania	923	2	Q55BF3_DICDI	Q55bf3 dictyosteli
851	7	0.9	654	2	Q62L07_BURMA	Q62l07 burkholderi	924	2	Q55BF3_DICDI	Q55bf3 dictyosteli
852	7	0.9	654	2	Q9SLA7_ARATH	Q9slaw7 arabidopsis	925	2	Q55BF3_DICDI	Q55bf3 dictyosteli
853	7	0.9	656	2	Q6L1S1_PHOPR	Q6l1s1 photobacter	926	2	Q55BF3_DICDI	Q55bf3 dictyosteli
854	7	0.9	659	2	Q4V584_DROME	Q4v584 drosophila	927	2	Q55BF3_DICDI	Q55bf3 dictyosteli
855	7	0.9	661	2	Q8D582_VIBVU	Q8d582 vibrio vuln	928	2	Q55BF3_DICDI	Q55bf3 dictyosteli
856	7	0.9	661	2	Q7MC29_VIBVY	Q7mc29 vibrio vuln	929	2	Q55BF3_DICDI	Q55bf3 dictyosteli
857	7	0.9	662	2	Q6XBJ0_MYCRH	Q6xbj0 mycobacteri	930	2	Q55BF3_DICDI	Q55bf3 dictyosteli
858	7	0.9	663	2	Q6BNA8_DEBHA	Q6bna8 debaryomyce	931	2	Q55BF3_DICDI	Q55bf3 dictyosteli
859	7	0.9	663	2	Q67T99_ARATH	Q67tn9 arabidopsis	932	2	Q55BF3_DICDI	Q55bf3 dictyosteli
860	7	0.9	663	2	Q8RWP2_ARATH	Q8rwp2 arabidopsis	933	2	Q55BF3_DICDI	Q55bf3 dictyosteli
861	7	0.9	663	2	Q940B9_ARATH	Q940b9 arabidopsis	934	2	Q55BF3_DICDI	Q55bf3 dictyosteli
862	7	0.9	663	2	Q56ZA8_ARATH	Q56za8 arabidopsis	935	2	Q55BF3_DICDI	Q55bf3 dictyosteli
863	7	0.9	663	2	Q5LQA7_SILPO	Q5lqa7 silicibacte	936	2	Q55BF3_DICDI	Q55bf3 dictyosteli
864	7	0.9	665	1	MTMR1_HUMAN	Q13613 homo sapien	937	2	Q55BF3_DICDI	Q55bf3 dictyosteli
865	7	0.9	666	2	Q9KKR7_VIBCH	Q9kk77 vibrio chol	938	2	Q55BF3_DICDI	Q55bf3 dictyosteli
866	7	0.9	666	2	Q9D9T9_BRAJA	Q9d9t9 bradyrhizob	939	2	Q55BF3_DICDI	Q55bf3 dictyosteli
867	7	0.9	674	2	Q4N615_THEPA	Q4n615 theileria p	940	2	Q55BF3_DICDI	Q55bf3 dictyosteli
868	7	0.9	680	2	Q8IMS5_DROME	Q8ims5 drosophila	941	2	Q55BF3_DICDI	Q55bf3 dictyosteli
869	7	0.9	682	2	Q5NPE2_ZYMOO	Q5npe2 zymomonas m	942	2	Q55BF3_DICDI	Q55bf3 dictyosteli
870	7	0.9	683	2	Q59Q14_CANAL	Q59q14 candida alb	943	2	Q55BF3_DICDI	Q55bf3 dictyosteli
871	7	0.9	684	2	Q75840_NEUCR	Q75840 neurospora	944	2	Q55BF3_DICDI	Q55bf3 dictyosteli
872	7	0.9	684	2	Q75840_NEUCR	Q75840 oryza sativ	945	2	Q55BF3_DICDI	Q55bf3 dictyosteli
873	7	0.9	685	2	Q65001_DICDI	Q65001 dictyosteli	946	2	Q55BF3_DICDI	Q55bf3 dictyosteli
874	7	0.9	687	2	Q5BBE4_EMENI	Q5bbe4 aspergillus	947	2	Q55BF3_DICDI	Q55bf3 dictyosteli
875	7	0.9	689	2	Q4NTX8_9DELT	Q4ntx8 anaeromyxob	948	2	Q55BF3_DICDI	Q55bf3 dictyosteli
876	7	0.9	693	2	Q63TE4_BURPS	Q63te4 burkholderi	949	2	Q55BF3_DICDI	Q55bf3 dictyosteli
877	7	0.9	695	2	Q8P8P4_PSEPK	Q8p8p4 pseudomonas	950	2	Q55BF3_DICDI	Q55bf3 dictyosteli
878	7	0.9	697	2	Q7QNS2_GIALA	Q7qns2 giardia lam	951	2	Q55BF3_DICDI	Q55bf3 dictyosteli
879	7	0.9	697	2	Q9VEP8_DROME	Q9vep8 drosophila	952	2	Q55BF3_DICDI	Q55bf3 dictyosteli
880	7	0.9	699	2	Q82E12_STRAW	Q82e12 streptomyce	953	2	Q55BF3_DICDI	Q55bf3 dictyosteli
881	7	0.9	701	2	Q4RK98_TETNG	Q4rk98 tetraodon n	954	2	Q55BF3_DICDI	Q55bf3 dictyosteli
882	7	0.9	702	2	Q8G6C8_BIFLO	Q8g6c8 bifidobacte	955	2	Q55BF3_DICDI	Q55bf3 dictyosteli
883	7	0.9	702	2	Q4S767_TETNG	Q4s767 tetraodon n	956	2	Q55BF3_DICDI	Q55bf3 dictyosteli
884	7	0.9	707	2	Q5P5D4_AZOSE	Q5p5d4 azoarcus sp	957	2	Q55BF3_DICDI	Q55bf3 dictyosteli
885	7	0.9	711	2	Q5BGO0_EMENI	Q5bgo0 aspergillus	958	2	Q55BF3_DICDI	Q55bf3 dictyosteli
886	7	0.9	712	2	Q52KF5_MOUSE	Q52kf5 mus musculus	959	2	Q55BF3_DICDI	Q55bf3 dictyosteli
887	7	0.9	713	2	Q5AVY0_EMENI	Q5avy0 aspergillus	960	2	Q55BF3_DICDI	Q55bf3 dictyosteli
888	7	0.9	717	2	Q9VAY0_DROME	Q9vay0 drosophila	961	2	Q55BF3_DICDI	Q55bf3 dictyosteli
889	7	0.9	718	2	Q7RPJ6_PLAYO	Q7rpj6 plasmodium	962	2	Q55BF3_DICDI	Q55bf3 dictyosteli
890	7	0.9	720	2	Q5IND5_MAGGR	Q5ind5 magnaporthe	963	2	Q55BF3_DICDI	Q55bf3 dictyosteli
891	7	0.9	721	2	Q52B74_MAGGR	Q52b74 magnaporthe	964	2	Q55BF3_DICDI	Q55bf3 dictyosteli
892	7	0.9	728	1	DGK1_ARATH	Q39017 arabidopsis	965	2	Q55BF3_DICDI	Q55bf3 dictyosteli
893	7	0.9	728	2	Q9VOY0_9HERP	Q9vyq0 ranid herpe	966	2	Q55BF3_DICDI	Q55bf3 dictyosteli
894	7	0.9	730	2	Q4WXK8_ASPFU	Q4wxk8 aspergillus	967	2	Q55BF3_DICDI	Q55bf3 dictyosteli
895	7	0.9	733	2	Q9UBZ1_HUMAN	Q9ubz1 homo sapien	968	2	Q55BF3_DICDI	Q55bf3 dictyosteli
896	7	0.9	733	2	Q5QA92_XANCV	Q5qa92 xanthomonas	969	2	Q55BF3_DICDI	Q55bf3 dictyosteli
897	7	0.9	734	2	Q7NP49_XANAC	Q7np49 xanthomonas	970	2	Q55BF3_DICDI	Q55bf3 dictyosteli
898	7	0.9	734	2	Q7NP49_XANAC	Q7np49 xanthomonas	971	2	Q55BF3_DICDI	Q55bf3 dictyosteli
899	7	0.9	741	2	Q4ZLP5_PSESE	Q4zlp5 pseudomonas	972	2	Q55BF3_DICDI	Q55bf3 dictyosteli
900	7	0.9	741	2	Q87UF7_PSESE	Q87uf7 pseudomonas	973	2	Q55BF3_DICDI	Q55bf3 dictyosteli
901	7	0.9	745	1	HGL2_ARATH	Q46807 arabidopsis	974	2	Q55BF3_DICDI	Q55bf3 dictyosteli
902	7	0.9	745	2	Q5AB99_CANAL	Q5ab99 candida alb	975	2	Q55BF3_DICDI	Q55bf3 dictyosteli
903	7	0.9	747	2	Q9C5F1_ARATH	Q9c5f1 arabidopsis	976	2	Q55BF3_DICDI	Q55bf3 dictyosteli
904	7	0.9	747	2	Q7P2X4_FUSNV	Q7p2x4 fusobacteri	977	2	Q55BF3_DICDI	Q55bf3 dictyosteli
905	7	0.9	750	2	Q8PHI0_XANAC	Q8phi0 xanthomonas	978	2	Q55BF3_DICDI	Q55bf3 dictyosteli
906	7	0.9	755	2	Q6K624_ORYSA	Q6k624 oryza sativ	979	2	Q55BF3_DICDI	Q55bf3 dictyosteli
907	7	0.9	756	2	Q751Y0_ASHGO	Q751y0 ashbya gos	980	2	Q55BF3_DICDI	Q55bf3 dictyosteli
908	7	0.9	758	2	Q5H419_XANOR	Q5h419 xanthomonas	981	2	Q55BF3_DICDI	Q55bf3 dictyosteli
909	7	0.9	758	2	Q5H6E3_XANOR	Q5h6e3 xanthomonas	982	2	Q55BF3_DICDI	Q55bf3 dictyosteli
910	7	0.9	759	2	Q9H2G6_HUMAN	Q9h2g6 bacteroides	983	2	Q55BF3_DICDI	Q55bf3 dictyosteli
911	7	0.9	761	2	Q9H2G6_HUMAN	Q9h2g6 bacteroides	984	2	Q55BF3_DICDI	Q55bf3 dictyosteli
912	7	0.9	763	2	Q55BF3_DICDI	Q55bf3 dictyosteli	985	2	Q55BF3_DICDI	Q55bf3 dictyosteli
913	7	0.9	771	2	Q55BF3_DICDI	Q55bf3 dictyosteli	986	2	Q55BF3_DICDI	Q55bf3 dictyosteli
914	7	0.9	771	2	Q55BF3_DICDI	Q55bf3 dictyosteli	987	2	Q55BF3_DICDI	Q55bf3 dictyosteli
915	7	0.9	771	2	Q55BF3_DICDI	Q55bf3 dictyosteli	988	2	Q55BF3_DICDI	Q55bf3 dictyosteli
916	7	0.9	771	2	Q55BF3_DICDI	Q55bf3 dictyosteli	989	2	Q55BF3_DICDI	Q55bf3 dictyosteli
917	7	0.9	773	2	Q55BF3_DICDI	Q55bf3 dictyosteli	990	2	Q55BF3_DICDI	Q55bf3 dictyosteli
918	7	0.9	773	2	Q55BF3_DICDI	Q55bf3 dictyosteli	991	2	Q55BF3_DICDI	Q55bf3 dictyosteli
919	7	0.9	774	2	Q55BF3_DICDI	Q55bf3 dictyosteli	992	2	Q55BF3_DICDI	Q55bf3 dictyosteli
920	7	0.9	778	2	Q55BF3_DICDI	Q55bf3 dictyosteli	993	2	Q55BF3_DICDI	Q55bf3 dictyosteli
921	7	0.9	784	2	Q55BF3_DICDI	Q55bf3 dictyosteli	994	2	Q55BF3_DICDI	Q55bf3 dictyosteli
922	7	0.9	784	2	Q55BF3_DICDI	Q55bf3 dictyosteli	995	2	Q55BF3_DICDI	Q55bf3 dictyosteli
923	7	0.9	784	2	Q55BF3_DICDI	Q55bf3 dictyosteli	996	2	Q55BF3_DICDI	Q55bf3 dictyosteli
924	7	0.9	786	2	Q55BF3_DICDI	Q55bf3 dictyosteli	997	2	Q55BF3_DICDI	Q55bf3 dictyosteli
925	7	0.9	786	2	Q55BF3_DICDI	Q55bf3 dictyosteli	998	2	Q55BF3_DICDI	Q55bf3 dictyosteli
926	7	0.9	788	2	Q55BF3_DICDI	Q55bf3 dictyosteli	999	2	Q55BF3_DICDI	Q55bf3 dictyosteli
927	7	0.9	790	2	Q55BF3_DICDI	Q55bf3 dictyosteli	1000	2	Q55BF3_DICDI	Q55bf3 dictyosteli
928	7	0.9	790	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
929	7	0.9	791	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
930	7	0.9	792	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
931	7	0.9	793	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
932	7	0.9	794	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
933	7	0.9	795	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
934	7	0.9	795	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
935	7	0.9	796	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
936	7	0.9	797	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
937	7	0.9	797	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
938	7	0.9	803	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
939	7	0.9	807	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
940	7	0.9	808	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
941	7	0.9	809	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
942	7	0.9	809	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
943	7	0.9	811	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
944	7	0.9	812	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
945	7	0.9	812	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
946	7	0.9	812	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
947	7	0.9	812	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
948	7	0.9	812	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
949	7	0.9	812	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
950	7	0.9	813	1	Q55BF3_DICDI	Q55bf3 dictyosteli				
951	7	0.9	813	1	Q55BF3_DICDI	Q55bf3 dictyosteli				
952	7	0.9	817	2	Q55BF3_DICDI	Q55bf3 dictyosteli				
9										

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981 7 0.9 876 2 04XV48 PLACH
982 7 0.9 876 2 05TL13_STRMU
983 7 0.9 876 2 04H729_9DEIO
984 7 0.9 883 2 06CRS9_kluyveromyc
985 7 0.9 885 2 08AJE1_BACTN
986 7 0.9 887 2 08XV49_RALSO
987 7 0.9 888 2 09L062_ARATH
988 7 0.9 889 2 05ILM3_MAIZE
989 7 0.9 893 2 06C3K8_YARLI
990 7 0.9 897 2 07KN84_DROME
991 7 0.9 897 2 09ULK2_DROME
992 7 0.9 897 2 09VZ26_DROME
993 7 0.9 899 2 05I411_NEIME
994 7 0.9 900 2 05IM51_MAGGR
995 7 0.9 916 2 09W354_DROME
996 7 0.9 916 2 05I410_NEIME
997 7 0.9 916 2 04SN22_TETNG
998 7 0.9 918 2 04VU88_9STRA
999 7 0.9 918 2 04VU87_9STRA
1000 7 0.9 921 2 05ZXL2_LEGPH

O4XV48 plasmodium
Q5tl13 streptococc
Q4h729 deinococcus
Q6crs9 kluyveromyc
Q8aje1 bacteroides
Q8xv49 ralstonia s
Q9lq62 arabidopsis
Q5yim3 zea mays (m
Q6c3k8 yarrowia li
Q7kn84 drosophila
Q9ulk2 drosophila
Q9vz26 drosophila
Q5i411 neisseria m
Q5lm51 magnaporthe
Q9w354 drosophila
Q5i410 neisseria m
Q4sn22 tetraodon n
Q4vu88 thalassiosl
Q4vu87 thalassiosl
Q5zx12 legionella

ALIGNMENTS

RESULT 1
O30912_NEIME PRELIMINARY; PRT; 797 AA.
ID O30912_NEIME PRELIMINARY; PRT; 797 AA.
AC O30912;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=Omp85;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HH;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Oma87.";
RL Microb. Pathog. 25:11-21(1998).
DR EMBL; AF021245; AAC17599.1; -; Genomic_DNA.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; -88539 MW; CF911B5F70B999CF CRC64;

Query Match 100.0%; Score 797; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQTASALMLGIGSLPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
DB 1 MKLKQTASALMLGIGSLPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
QY 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLSEFLAQ 120
DB 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLSEFLAQ 120
QY 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
DB 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
QY 181 FEGNOVYSDRKLRQMSLTGGIWTLTRSNQFNQKFAQDMKVTDFYQNNGYPDFRIL 240
DB 181 FEGNOVYSDRKLRQMSLTGGIWTLTRSNQFNQKFAQDMKVTDFYQNNGYPDFRIL 240

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DB 181 FEGNOVYSDRKLRQMSLTGGIWTLTRSNQFNQKFAQDMKVTDFYQNNGYPDFRIL 240
QY 241 DTIDIQTNEKTKQTITKITVHEGGRFRWKVSTEGDTNEVPKAELEKLLTMKPGKMYEROQ 300
DB 241 DTIDIQTNEKTKQTITKITVHEGGRFRWKVSTEGDTNEVPKAELEKLLTMKPGKMYEROQ 300
QY 301 MTAVLGEIQNRMGSAAYSEISVQPLNPAETKTVDVFLVHIEPGRKIYVNEIHTIGNNKT 360
DB 301 MTAVLGEIQNRMGSAAYSEISVQPLNPAETKTVDVFLVHIEPGRKIYVNEIHTIGNNKT 360
QY 361 RDEVVRRELROMESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNMSLTE 420
DB 361 RDEVVRRELROMESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNMSLTE 420
QY 421 RSTGSLDLISAGVWQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGLSFTDPFYFTA 480
DB 421 RSTGSLDLISAGVWQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGLSFTDPFYFTA 480
QY 481 DGVSLGYDVGKAFDPKPKASTSIKQYKTTTACAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGYDVGKAFDPKPKASTSIKQYKTTTACAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKTKDGTGSPKGLYKGTVGWRNKTDTSALMPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKTKDGTGSPKGLYKGTVGWRNKTDTSALMPTRGYLTGVNAEIA 600
QY 601 LPGSKLQYYSAATHNQTPFPPLSKTFTTLMGGVEGVIAGGYGRYKEIPFFNFYGGGLGSVR 660
DB 601 LPGSKLQYYSAATHNQTPFPPLSKTFTTLMGGVEGVIAGGYGRYKEIPFFNFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGNKANKVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGNKANKVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQGTTF 797
DB 781 KPEDEIQRFQFQGTTF 797

RESULT 2
Q9UXJ31_NEIMA PRELIMINARY; PRT; 797 AA.
ID Q9UXJ31_NEIMA PRELIMINARY; PRT; 797 AA.
AC Q9JX31;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocuNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162752; CAB83401.1; -; Genomic_DNA.
DR PIR; D82000; D82000.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR000184; Bac_surfAg_D15.

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Qy 621 LSKTFTLMLGGEVCIAGYGRTRKEIPFFENFYGGGLSGVRGYSGLTGPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVCIAGYGRTRKEIPFFENFYGGGLSGVRGYSGLTGPKVYDEYGEKIS 680
Qy 681 YGGNKKANVAEELFFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVONIYG 740
Db 681 YGGNKKANVAEELFFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVONIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772

RESULT 4
QSF5W8_NEIG1
ID QSF5W8_NEIG1 PRELIMINARY; PRT; 792 AA.
AC QSF5W8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=NGO1801;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najaf F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE004969; AAW90419.1: -; Genomic_DNA.
DR InterPro: IPR00184; Bac surfAg D15.
DR Pfam: PF01103; Bac surface Ag; 1.
DR Pfam: PF07244; Surf Ag VNR; 5.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 792 AA; 87942 MW; 8EB06CA369C15812 CRC64;

Query Match 26.3%; Score 210; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 9.2e-211;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMWLGISPLAFADFTIQRVEGLQRTPESTFVNYLPVKVGDTYNDTHGSA 60
Db 1 MKLQIASALMWLGISPLAFADFTIQRVEGLQRTPESTFVNYLPVKVGDTYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLTIVERTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLTIVERTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
Qy 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQTTPKVKTLARNRVIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQTTPKVKTLARNRVIDITIDEGKSAKITDIE 180
Qy 181 FEGNQVYSDRKLQRQNSLTGGGIWTWLTLS 210
Db 181 FEGNQVYSDRKLQRQNSLTGGGIWTWLTLS 210

RESULT 5
P95359_NEIGO
ID P95359_NEIGO PRELIMINARY; PRT; 792 AA.
AC P95359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN Name=omp85;
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OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=FA19;
RC MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RX Manning D.S., Reschke D.K., Judd R.C.;
RA "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
RT are similar to Haemophilus influenzae D-15-Ag and Pasteurella
RL multocida Oms87."
RL Microb. Pathog. 25:11-21(1998).
DR EMBL: U81959; AAC17600.1: -; Genomic_DNA.
DR GO: GO:0019867; C:outer membrane; IEA.
DR InterPro: IPR000184; Bac surfAg D15.
DR InterPro: IPR010827; Surf Ag VNR.
DR Pfam: PF01103; Bac surface Ag; 1.
DR Pfam: PF07244; Surf Ag VNR; 5.
SQ SEQUENCE 792 AA; 87868 MW; 90E32D24AA0513D8 CRC64;

Query Match 19.7%; Score 157; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 4.7e-155;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDVFLHIEFGKLYVNEIHTGNKTRDEVVRELQMESAPYDTSKLQSKERVEL 391
Db 332 TKTVDVFLHIEFGKLYVNEIHTGNKTRDEVVRELQMESAPYDTSKLQSKERVEL 391
Qy 392 LGVFDNVQDVLPLAGTDPKVDLNSLTERSTGSLDLSAGVQDQTLGVNSAGVSQDNLFG 451
Db 392 LGVFDNVQDVLPLAGTDPKVDLNSLTERSTGSLDLSAGVQDQTLGVNSAGVSQDNLFG 451
Qy 452 TGKSAALRASRKTTLNGSLSTFDPYFTADGVSGLYD 488
Db 452 TGKSAALRASRKTTLNGSLSTFDPYFTADGVSGLYD 488

RESULT 6
Q7NVY6_CHRVO
ID Q7NVY6_CHRVO PRELIMINARY; PRT; 771 AA.
AC Q7NVY6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable outer membrane protein.
GN OrderedLocusNames=CV2204;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=ATCC 12472 / DSM 30191;
RC MEDLINE=22882680; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RX Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Atolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Gribard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
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DB 474 DPYFTADGVSGLGY 486

RESULT 8
Q88H14_PSEPK
ID Q88H14_PSEPK PRELIMINARY; PRT; 787 AA.
AC Q88H14_7
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bacterial surface antigen family protein.
GN OrderedLocusNames=PP3373;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
RX NCBI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL MEDLINE=22423060; PubMed=12534463;
DOI=10.1046/j.1462-9290.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duisterhoef A., Tummlier B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR ENML; AS016786; AAN68977.1; -; Genomic_DNA.
DR TIGR; PP3373; -.
DR GO; GO:0019867; C:outer membrane; IEA.
DR InterPro; IPR000184; Bac surfAg D15.
DR DR InterPro: IPR010827; Surf_Ag_VNR.
DR Pfam; PR01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 787 AA; 86513 MW; 41FE0C4E311A6A97 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 787;
Best Local Similarity 100.0%; Pred.No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 475 DPYFTADGVSGLGY 487
|||||
DB 474 DPYFTADGVSGLGY 486
|||||

RESULT 9
Q8XZ13_RALSO
ID Q8XZ13_RALSO PRELIMINARY; PRT; 765 AA.
AC Q8XZ13_7
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.
GN OrderedLocusNames=RSC1412; ORFNames=RS05280;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
RX NCBI_TaxID=305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL STAIN=GMI1000.
RA MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Arriaguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billaut A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choigne N., Claudel-Renard C., Cunne S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.

RA Weissenbach J., Boucher C.A.;
 RT "genome sequence of the plant pathogen Ralstonia solanacearum."
 RL Nature 415:497-502(2002).
 DR EMBL; AL646064; CAD15114.1; -; Genomic_DNA.
 GO; GO:0019867; C:outer membrane; IEA.
 DR InterPro; IPR002198; ADH short.
 DR InterPro; IPR000184; Bac_surfAg_D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac_surface_Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 DR PROSITE; PS00061; ADH_SHORT; UNKNOWN 1.
 KW Complete proteome.
 SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 1.3%; Score 10; DB 2; Length 765;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 KTRDEVVRRE 368

DB 365 KTRDEVVRRE 374

RESULT 10

Q5NZG7_AZOSE PRELIMINARY; PRT; 766 AA.

AC Q5NZG7;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DE Probable outer membrane protein/surface antigen.

GN OrderedLocuNames=AZOSEA4220; ORFNames=eBA5996;

OS Azocarcus sp. (strain EBN1).

OC Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales;

OC Rhodocyclaceae; Azocarcus.

OX NCBI_TaxID=76114;

RP [1]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=EBN1;

RX PubMed=15551059; DOI=10.1007/s00203-004-0742-9;

RA Rabus R., Kube M., Heider J., Beck A., Heitmann K., Widdel F.,

RA Reinhardt R.;

RT "the genome sequence of an anaerobic aromatic-degrading denitrifying

RT bacterium, strain EBN1.";

RL Arch. Microbiol. 183:27-36(2005).

DR EMBL; CR555306; CAI09547.1; -; Genomic_DNA.

DR GO; GO:0019867; C:outer membrane; IEA.

DR InterPro; IPR000184; Bac_surfAg_D15.

DR InterPro; IPR010827; Surf_Ag_VNR.

DR Pfam; PF01103; Bac_surface_Ag; 1.

DR Pfam; PF07244; Surf_Ag_VNR; 5.

KW Complete proteome.

SQ SEQUENCE 766 AA; 85845 MW; 3C7AA8475E5C8CB2 CRC64;

Query Match 1.3%; Score 10; DB 2; Length 766;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 KTRDEVVRRE 368

DB 360 KTRDEVVRRE 369

RESULT 11

Q9SMN7_ARATH PRELIMINARY; PRT; 328 AA.

ID Q9SMN7_ARATH

AC Q9SMN7;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein T8P19.130.

GN Name=T8P19.130;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RP NUCLEOTIDE SEQUENCE.
 RA Choiane N., Robert C., Brottier P., Wincker P., Cattolico L.,
 RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X., Quetier F., Salanoubat M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]

RN NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL133315; CAB62351.1; -; Genomic_DNA.

DR PIR; T46206; T46206.

DR InterPro; IPR000184; Bac_surfAg_D15.

DR Pfam; PF01103; Bac_surface_Ag; 1.

KW Hypothetical protein.

SQ SEQUENCE 328 AA; 36233 MW; CDB4D2B1EA2530C6 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 328;

Best Local Similarity 100.0%; Pred. No. 7.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGVRGY 662

DB 152 GGLGVRGY 160

RESULT 12

Q6L543_ORYSA PRELIMINARY; PRT; 361 AA.

ID Q6L543_ORYSA

AC Q6L543;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein OJ1005_B11.2.

GN Names=OJ1005_B11.2;

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,

RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,

RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,

RA Haiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,

RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,

RA Wu H.-P., Shaw J.-F.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC108873; AAT44133.1; -; Genomic_DNA.

DR Gramene; Q6L543; -.

DR InterPro; IPR000184; Bac_surfAg_D15.

DR Pfam; PF01103; Bac_surface_Ag; 1.

KW Hypothetical protein.

SQ SEQUENCE 361 AA; 38699 MW; 2737C18E5F63779E CRC64;

Query Match 1.1%; Score 9; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 8.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGVRGY 662

DB 255 GGLGVRGY 263

RESULT 13

Q5PP51_ARATH PRELIMINARY; PRT; 362 AA.

ID Q5PP51_ARATH

AC Q5PP51;

DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE At3g944160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN NUCLEOTIDE SEQUENCE.
RP Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RA "Arabidopsis ORF clones."
RT Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
RL [2]
RN NUCLEOTIDE SEQUENCE.
RP Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RA "Arabidopsis ORF clones."
RT Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; BT020246; ANV74240.1; -; mRNA.
DR EMBL; BT021139; AAX22274.1; -; mRNA.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR Pfam; PF01103; Bac_surface_Ag; 1.
SQ SEQUENCE 362 AA; 39010 MW; 383B1596A41F660A CRC64;

Query Match 1.1%; Score 9; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSRVGY 662
Db 255 GGLGSRVGY 263
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RESULT 14
Q9LXP7_ARATH PRELIMINARY; PRT; 435 AA.
ID Q9LXP7_ARATH PRELIMINARY; PRT; 435 AA.
AC Q9LXP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F26G5_110.
GN Name=F26G5_110;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL353814; CAB88424.1; -; Genomic_DNA.
DR PIR; T49132; T49132.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR Pfam; PF01103; Bac_surface_Ag; 1.
KW Hypothetical protein.
SQ SEQUENCE 435 AA; 47528 MW; C148B36074E49427 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSRVGY 662
Db 296 GGLGSRVGY 304
|||||

RESULT 15
Q9ZAE1_THETH PRELIMINARY; PRT; 713 AA.
ID Q9ZAE1_THETH PRELIMINARY; PRT; 713 AA.
AC Q9ZAE1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polynucleotide phosphorylase.
GN Name=pnp;
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=VK1;
RC Sarganov A.A., Garber M.B., Portier C.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; Z84207; CAB06341.1; -; Genomic_DNA.
DR HSP; P05055; ISRO.
DR GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR001247; 3-Exonase.
DR InterPro; IPR004087; KH.
DR InterPro; IPR004088; KH_type_1.
DR InterPro; IPR003029; S1_1.
DR Pfam; PF00013; KH_1; 1.
DR Pfam; PF03726; PNPase; 1.
DR Pfam; PF01138; RNase_PH; 2.
DR Pfam; PF03725; RNase_PH_C; 2.
DR Pfam; PF00575; S1_1.
DR SMART; SM00322; KH; 1.
DR SMART; SM00316; S1_1.
DR PROSITE; PSS0084; KH_TYPE_1; 1.
DR PROSITE; PSS0126; S1_1.
SQ SEQUENCE 713 AA; 78192 MW; 2979859D9AC5EA82 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 362 DEVVRREL 370
Db 310 DEVVRREL 318
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Search completed: April 12, 2006, 16:23:17
Job time : 282 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 12, 2006, 16:35:33 ; Search time 28 Seconds
(without alignments)
1209.426 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797
Sequence: 1 MKLKQIASALMLGISPLAF.....LKKKPEDEIQRFQJGTTTF 797

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 217505 seqs, 42489236 residues

Word size : 1

Total number of hits satisfying chosen parameters: 217077

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA New:*

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- 2: /SIDSS/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS/prodata/2/pubpaa/ECT_NEW_PUB.pep.*
- 5: /SIDSS/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 6: /SIDSS/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /SIDSS/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /SIDSS/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	210	26.3	792 6	US-10-467-657-6026 Sequence 6026, Ap
2	210	26.3	792 6	US-10-467-657-7528 Sequence 7528, Ap
3	157	19.7	792 7	US-11-103-957-92 Sequence 92, Appl
4	7	0.9	102 6	US-10-506-454-1658 Sequence 1658, Ap
5	7	0.9	147 7	US-11-158-655-6 Sequence 6, Appl
6	7	0.9	157 7	US-11-087-099-3827 Sequence 3827, Ap
7	7	0.9	177 7	US-11-172-740-872 Sequence 872, Appl
8	7	0.9	222 7	US-11-096-568A-1873 Sequence 1873, Ap
9	7	0.9	222 7	US-11-096-568A-27201 Sequence 27201, A
10	7	0.9	238 7	US-11-188-298-16796 Sequence 16796, A
11	7	0.9	241 7	US-11-096-568A-1872 Sequence 1872, Ap
12	7	0.9	241 7	US-11-096-568A-27200 Sequence 27200, A
13	7	0.9	286 7	US-11-079-463-6578 Sequence 6578, Ap
14	7	0.9	287 7	US-11-096-568A-18041 Sequence 18041, A
15	7	0.9	308 7	US-11-188-298-10985 Sequence 10985, A
16	7	0.9	346 7	US-11-098-686-10717 Sequence 10717, A
17	7	0.9	349 7	US-11-079-463-10148 Sequence 10148, A
18	7	0.9	352 7	US-11-051-720-1325 Sequence 1325, Ap
19	7	0.9	354 7	US-11-051-720-1324 Sequence 1324, Ap
20	7	0.9	363 7	US-11-087-099-7789 Sequence 7789, Ap
21	7	0.9	363 7	US-11-051-720-1326 Sequence 1326, Ap
22	7	0.9	363 7	US-11-188-298-7183 Sequence 7183, Ap
23	7	0.9	364 7	US-11-087-099-5056 Sequence 5056, Ap
24	7	0.9	364 7	US-11-188-298-15670 Sequence 15670, A
25	7	0.9	366 7	US-11-188-298-1324 Sequence 1324, Ap

366	7	0.9	7	US-11-188-298-17268	Sequence 17268, A
377	7	0.9	7	US-11-124-368A-209	Sequence 209, App
377	7	0.9	7	US-11-124-368A-210	Sequence 210, App
384	7	0.9	7	US-11-087-099-6378	Sequence 6378, Ap
384	7	0.9	7	US-11-188-298-16869	Sequence 16869, A
398	7	0.9	7	US-11-188-298-12144	Sequence 12144, A
399	7	0.9	7	US-11-188-298-13100	Sequence 13100, A
453	7	0.9	7	US-11-096-568A-18040	Sequence 18040, A
462	7	0.9	7	US-11-096-568A-12044	Sequence 12044, A
472	7	0.9	7	US-11-096-568A-12043	Sequence 12043, A
472	7	0.9	7	US-11-096-568A-18039	Sequence 18039, A
494	7	0.9	7	US-11-024-959-445	Sequence 445, App
512	7	0.9	7	US-11-188-298-19322	Sequence 19322, A
517	7	0.9	7	US-11-051-720-1432	Sequence 1432, Ap
549	7	0.9	7	US-11-085-185-2	Sequence 2, Appli
564	7	0.9	7	US-11-096-568A-12042	Sequence 12042, A
564	7	0.9	7	US-11-188-298-3110	Sequence 3110, Ap
569	7	0.9	7	US-11-188-298-789	Sequence 789, App
572	6	0.9	6	US-10-204-639-14	Sequence 14, Appl
572	7	0.9	7	US-11-188-298-582	Sequence 582, App
575	7	0.9	7	US-11-188-298-17173	Sequence 17173, A
575	7	0.9	7	US-11-188-298-22207	Sequence 22207, A
639	7	0.9	7	US-11-188-298-13558	Sequence 13558, A
666	7	0.9	7	US-11-055-822-48	Sequence 48, Appl
745	7	0.9	7	US-11-147-109-2	Sequence 2, Appli
830	6	0.9	6	US-10-921-793-38	Sequence 38, Appl
830	7	0.9	7	US-10-931-198-38	Sequence 38, Appl
830	6	0.9	6	US-10-942-042-38	Sequence 38, Appl
839	7	0.9	7	US-11-079-463-8849	Sequence 8849, Ap
1390	7	0.9	7	US-11-063-343-35	Sequence 35, Appl
1449	7	0.9	7	US-11-052-554A-237	Sequence 237, App
1458	7	0.9	7	US-11-096-274-2	Sequence 2, Appli
1468	6	0.9	6	US-10-467-657-1088	Sequence 1088, Ap
1892	7	0.9	7	US-11-075-185-6	Sequence 6, Appli
2431	6	0.9	6	US-10-958-267-6	Sequence 6, Appli
2431	6	0.9	6	US-10-958-267-8	Sequence 8, Appli
2432	6	0.9	6	US-10-958-267-12	Sequence 12, Appl
2432	6	0.9	6	US-10-958-267-12	Sequence 12, Appl
3194	7	0.9	7	US-11-052-554A-90	Sequence 90, Appl
3655	7	0.9	7	US-11-075-185-5	Sequence 5, Appli
3689	7	0.9	7	US-11-075-185-4	Sequence 4, Appli
6893	7	0.9	7	US-11-205-109-14	Sequence 14, Appl
15	7	0.8	7	US-11-054-515-2970	Sequence 2970, Ap
15	7	0.8	7	US-11-266-444-2970	Sequence 2970, Ap
18	7	0.8	7	US-11-119-581-76	Sequence 76, Appl
31	7	0.8	7	US-11-035-826-247	Sequence 247, App
34	6	0.8	6	US-10-516-224-5	Sequence 5, Appli
34	6	0.8	6	US-10-516-224-7	Sequence 7, Appli
40	7	0.8	7	US-11-119-249-13	Sequence 13, Appli
54	7	0.8	7	US-11-004-399-2597	Sequence 2597, Ap
60	7	0.8	7	US-11-079-463-7905	Sequence 7905, Ap
60	7	0.8	7	US-11-079-463-8104	Sequence 8104, Ap
60	7	0.8	7	US-11-079-463-10066	Sequence 10066, A
72	7	0.8	7	US-11-188-298-21799	Sequence 21799, A
75	6	0.8	6	US-10-467-657-7058	Sequence 7058, Ap
78	6	0.8	6	US-10-467-657-7058	Sequence 7058, Ap
78	6	0.8	6	US-10-506-454-1042	Sequence 1042, Ap
79	7	0.8	7	US-11-079-463-5673	Sequence 5673, Ap
85	7	0.8	7	US-11-079-463-8244	Sequence 8244, Ap
91	7	0.8	7	US-11-096-568A-2211	Sequence 2211, Ap
94	6	0.8	6	US-10-467-657-3628	Sequence 3628, Ap
94	6	0.8	6	US-10-467-657-6394	Sequence 6394, Ap
94	6	0.8	6	US-11-096-568A-2205	Sequence 2205, Ap
95	7	0.8	7	US-11-096-568A-1030	Sequence 1030, Ap
95	7	0.8	7	US-11-079-463-7733	Sequence 7733, Ap
96	6	0.8	6	US-11-087-099-3171	Sequence 3171, Ap
99	7	0.8	7	US-11-107-096-79	Sequence 79, Appl
99	7	0.8	7	US-11-096-568A-2210	Sequence 2210, Ap
99	7	0.8	7	US-11-188-298-3758	Sequence 3758, Ap
100	7	0.8	7	US-11-096-568A-2479	Sequence 2479, Ap
103	7	0.8	7	US-11-096-568A-9403	Sequence 9403, Ap
104	6	0.8	6	US-10-501-035-356	Sequence 356, App
105	7	0.8	7	US-11-188-298-13304	Sequence 13304, A

99	6	0.8	106	6	US-10-507-662-42	Sequence 42, Appl	172	6	0.8	175	7	US-11-087-099-4823	Sequence 4823, Ap
100	6	0.8	106	6	US-10-507-662-43	Sequence 43, Appl	173	6	0.8	175	7	US-11-087-099-9423	Sequence 9423, Ap
101	6	0.8	106	7	US-11-152-846-8	Sequence 8, Appli	174	6	0.8	179	7	US-11-096-568A-1165	Sequence 1165, Ap
102	6	0.8	106	7	US-11-152-846-10	Sequence 10, Appl	175	6	0.8	180	7	US-11-096-568A-9402	Sequence 9402, Ap
103	6	0.8	106	7	US-11-183-205-38	Sequence 38, Appl	176	6	0.8	182	7	US-11-052-554A-5	Sequence 5, Appli
104	6	0.8	106	7	US-11-250-411-98	Sequence 98, Appl	177	6	0.8	183	7	US-11-188-298-1411	Sequence 1411, A
105	6	0.8	106	7	US-11-250-411-103	Sequence 103, App	178	6	0.8	186	6	US-10-467-657-6312	Sequence 6312, Ap
106	6	0.8	107	7	US-11-221-900-6	Sequence 6, Appli	179	6	0.8	186	7	US-11-087-099-9087	Sequence 9087, Ap
107	6	0.8	107	7	US-11-221-900-8	Sequence 8, Appli	180	6	0.8	187	7	US-11-186-284-195	Sequence 195, App
108	6	0.8	107	7	US-11-221-900-9	Sequence 9, Appli	181	6	0.8	188	7	US-11-087-099-4563	Sequence 4563, Ap
109	6	0.8	107	7	US-11-284-260-25	Sequence 25, Appl	182	6	0.8	188	7	US-11-087-099-6041	Sequence 6041, Ap
110	6	0.8	107	7	US-11-284-260-26	Sequence 26, Appl	183	6	0.8	189	7	US-11-087-099-8115	Sequence 8115, Ap
111	6	0.8	107	7	US-11-284-260-27	Sequence 27, Appl	184	6	0.8	189	7	US-11-188-298-2510	Sequence 2510, Ap
112	6	0.8	107	7	US-11-284-260-28	Sequence 28, Appl	185	6	0.8	189	7	US-11-188-298-15781	Sequence 15781, A
113	6	0.8	107	7	US-11-284-260-29	Sequence 29, Appl	186	6	0.8	190	7	US-11-087-099-4780	Sequence 4780, Ap
114	6	0.8	107	7	US-11-284-260-29	Sequence 25, Appl	187	6	0.8	191	7	US-11-087-099-8028	Sequence 8028, Ap
115	6	0.8	107	7	US-11-284-261-25	Sequence 26, Appl	188	6	0.8	192	7	US-11-188-298-20652	Sequence 20652, A
116	6	0.8	107	7	US-11-284-261-26	Sequence 27, Appl	189	6	0.8	193	6	US-10-467-657-540	Sequence 540, App
117	6	0.8	107	7	US-11-284-261-27	Sequence 28, Appl	190	6	0.8	193	7	US-11-096-568A-24647	Sequence 24647, A
118	6	0.8	107	7	US-11-284-261-28	Sequence 29, Appl	191	6	0.8	193	7	US-11-188-298-4266	Sequence 4266, Ap
119	6	0.8	109	7	US-11-171-567-207	Sequence 207, App	192	6	0.8	193	7	US-11-188-298-21647	Sequence 21647, A
120	6	0.8	110	7	US-11-193-512-33	Sequence 33, Appl	193	6	0.8	195	7	US-11-079-463-7447	Sequence 7447, Ap
121	6	0.8	111	7	US-11-096-568A-1029	Sequence 1029, Ap	194	6	0.8	196	7	US-11-087-099-11349	Sequence 11349, A
122	6	0.8	112	6	US-10-793-626-2114	Sequence 2114, Ap	195	6	0.8	197	7	US-11-215-658-7	Sequence 7, Appli
123	6	0.8	112	7	US-11-188-298-13284	Sequence 13284, A	196	6	0.8	197	7	US-11-096-568A-20126	Sequence 20126, A
124	6	0.8	114	6	US-10-793-626-2252	Sequence 2252, Ap	197	6	0.8	198	7	US-11-186-284-101	Sequence 101, App
125	6	0.8	115	7	US-11-098-686-10642	Sequence 10642, A	198	6	0.8	198	7	US-11-051-724-54	Sequence 54, Appl
126	6	0.8	116	7	US-11-096-568A-6413	Sequence 6413, Ap	199	6	0.8	198	7	US-11-051-724-56	Sequence 56, Appl
127	6	0.8	116	7	US-11-079-463-6970	Sequence 6970, Ap	200	6	0.8	200	7	US-11-188-298-496	Sequence 496, App
128	6	0.8	117	7	US-11-087-099-8754	Sequence 8754, Ap	201	6	0.8	202	7	US-11-096-568A-11688	Sequence 11688, A
129	6	0.8	117	7	US-11-188-298-303	Sequence 303, App	202	6	0.8	203	7	US-11-098-686-10829	Sequence 10829, A
130	6	0.8	121	6	US-10-644-807-258	Sequence 72, Appl	203	6	0.8	203	7	US-11-188-298-8291	Sequence 8291, Ap
131	6	0.8	122	6	US-10-644-807-357	Sequence 357, App	204	6	0.8	204	6	US-10-793-626-2394	Sequence 2394, Ap
132	6	0.8	122	6	US-11-096-568A-628	Sequence 628, App	205	6	0.8	204	7	US-11-052-554A-377	Sequence 377, App
133	6	0.8	126	7	US-11-355-775-54	Sequence 54, Appl	206	6	0.8	204	7	US-11-096-568A-747	Sequence 747, App
134	6	0.8	128	7	US-11-250-411-82	Sequence 82, Appl	207	6	0.8	205	6	US-10-793-626-3020	Sequence 3020, Ap
135	6	0.8	128	7	US-11-250-411-97	Sequence 97, Appl	208	6	0.8	206	7	US-11-098-686-10732	Sequence 10732, A
136	6	0.8	128	7	US-11-250-411-98	Sequence 92, Appl	209	6	0.8	206	7	US-11-096-568A-16113	Sequence 16113, A
137	6	0.8	131	6	US-10-506-454-130	Sequence 130, App	210	6	0.8	206	7	US-11-096-568A-20184	Sequence 20184, A
138	6	0.8	131	7	US-11-096-568A-1028	Sequence 1028, Ap	211	6	0.8	207	7	US-11-096-568A-3970	Sequence 3970, Ap
139	6	0.8	134	7	US-11-072-512-2098	Sequence 2098, Ap	212	6	0.8	207	7	US-11-096-568A-9401	Sequence 9401, Ap
140	6	0.8	135	7	US-11-096-568A-23609	Sequence 23609, A	213	6	0.8	207	7	US-11-096-568A-9404	Sequence 9404, Ap
141	6	0.8	137	7	US-11-079-463-9914	Sequence 9914, Ap	214	6	0.8	208	7	US-11-129-104-97	Sequence 97, Appl
142	6	0.8	138	7	US-11-128-900-79	Sequence 79, Appl	215	6	0.8	210	7	US-11-188-298-13771	Sequence 13771, A
143	6	0.8	141	7	US-11-087-099-7283	Sequence 7283, Ap	216	6	0.8	210	7	US-11-188-298-15851	Sequence 15851, A
144	6	0.8	143	7	US-11-087-099-9821	Sequence 9821, Ap	217	6	0.8	211	7	US-11-098-686-11200	Sequence 11200, A
145	6	0.8	143	7	US-11-096-568A-1166	Sequence 1166, Ap	218	6	0.8	213	7	US-11-102-621-135	Sequence 135, App
146	6	0.8	144	7	US-11-072-512-3457	Sequence 3457, Ap	219	6	0.8	215	7	US-11-188-298-22562	Sequence 22562, A
147	6	0.8	144	7	US-11-087-099-12215	Sequence 12215, A	220	6	0.8	216	7	US-11-087-099-13335	Sequence 12335, A
148	6	0.8	144	7	US-11-096-568A-23608	Sequence 23608, A	221	6	0.8	216	7	US-11-096-568A-18899	Sequence 18899, A
149	6	0.8	146	7	US-11-087-099-8355	Sequence 8355, Ap	222	6	0.8	218	7	US-11-096-568A-13651	Sequence 13651, A
150	6	0.8	150	5	US-09-978-360A-708	Sequence 708, App	223	6	0.8	219	6	US-10-518-019A-6	Sequence 6, Appli
151	6	0.8	150	7	US-11-188-298-9339	Sequence 9339, Ap	224	6	0.8	219	7	US-11-087-099-8268	Sequence 8268, Ap
152	6	0.8	154	7	US-11-052-554A-327	Sequence 327, App	225	6	0.8	223	6	US-10-508-263-119	Sequence 119, App
153	6	0.8	155	7	US-11-087-099-3541	Sequence 3541, Ap	226	6	0.8	225	6	US-10-793-626-1594	Sequence 1594, Ap
154	6	0.8	155	7	US-11-096-568A-627	Sequence 627, App	227	6	0.8	226	7	US-11-188-298-21324	Sequence 21324, A
155	6	0.8	157	7	US-11-087-099-4136	Sequence 4136, Ap	228	6	0.8	229	7	US-11-188-298-11181	Sequence 11181, A
156	6	0.8	158	7	US-11-079-463-6106	Sequence 6106, Ap	229	6	0.8	231	7	US-11-096-568A-7771	Sequence 7771, Ap
157	6	0.8	158	7	US-11-188-298-4807	Sequence 4807, Ap	230	6	0.8	233	7	US-11-087-099-1395	Sequence 1395, Ap
158	6	0.8	159	7	US-11-087-099-5905	Sequence 5905, Ap	231	6	0.8	234	7	US-11-188-298-19658	Sequence 19658, A
159	6	0.8	159	7	US-11-051-724-58	Sequence 58, Appl	232	6	0.8	235	7	US-11-096-568A-18863	Sequence 18863, A
160	6	0.8	160	7	US-11-057-012-7	Sequence 7, Appli	233	6	0.8	235	7	US-11-284-260-5	Sequence 5, Appli
161	6	0.8	160	7	US-10-714-887-2161	Sequence 2161, Ap	234	6	0.8	236	7	US-11-087-099-11734	Sequence 11734, A
162	6	0.8	161	6	US-11-215-658-8	Sequence 294, App	235	6	0.8	236	7	US-11-096-568A-16112	Sequence 16112, A
163	6	0.8	162	7	US-11-096-568A-14219	Sequence 8, Appli	236	6	0.8	236	7	US-11-096-568A-27570	Sequence 27570, A
164	6	0.8	162	7	US-10-475-075-803	Sequence 803, App	237	6	0.8	236	7	US-11-096-568A-29000	Sequence 29000, A
165	6	0.8	165	6	US-10-506-454-824	Sequence 21132, A	238	6	0.8	239	7	US-11-000-463-875	Sequence 875, App
166	6	0.8	166	6	US-10-506-454-824	Sequence 824, App	239	6	0.8	239	7	US-11-000-463-876	Sequence 876, App
167	6	0.8	167	7	US-11-096-568A-3391	Sequence 3391, Ap	240	6	0.8	239	7	US-11-096-568A-7433	Sequence 7433, Ap
168	6	0.8	172	7	US-11-096-568A-5913	Sequence 5913, Ap	241	6	0.8	239	7	US-11-096-568A-32542	Sequence 32542, A
169	6	0.8	172	7	US-11-096-568A-31907	Sequence 31907, A	242	6	0.8	240	7	US-11-096-568A-24894	Sequence 24894, A
170	6	0.8	173	7	US-11-079-463-6942	Sequence 6942, Ap	243	6	0.8	241	6	US-10-878-556A-35	Sequence 35, Appl
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245	6	0.8	242	7	US-11-188-298-6437	Sequence 6437, Ap	318	264	7	US-11-096-568A-25556	Sequence 25556, A
246	6	0.8	243	6	US-10-506-454-277	Sequence 277, App	319	265	7	US-11-072-512-2141	Sequence 2141, Ap
247	6	0.8	243	7	US-11-096-568A-7432	Sequence 7432, Ap	320	266	7	US-11-098-686-10476	Sequence 10476, A
248	6	0.8	243	7	US-11-096-568A-9662	Sequence 9662, Ap	321	267	6	US-10-501-035-293	Sequence 293, App
249	6	0.8	243	7	US-11-096-568A-18898	Sequence 18898, A	322	267	6	US-10-506-454-380	Sequence 380, App
250	6	0.8	243	7	US-11-096-568A-24644	Sequence 24644, A	323	267	7	US-11-096-568A-9661	Sequence 9661, Ap
251	6	0.8	244	6	US-10-467-657-8278	Sequence 8278, Ap	324	269	7	US-11-000-463-403	Sequence 403, App
252	6	0.8	244	7	US-11-096-568A-27569	Sequence 27569, Ap	325	269	7	US-11-224-726-1	Sequence 1, Appli
253	6	0.8	244	7	US-11-096-568A-31975	Sequence 31975, A	326	271	6	US-10-467-657-7690	Sequence 7690, Ap
254	6	0.8	244	7	US-11-079-463-8622	Sequence 8622, Ap	327	273	7	US-11-070-080-19	Sequence 19, Appl
255	6	0.8	244	7	US-11-079-463-9308	Sequence 9308, Ap	328	273	7	US-11-096-568A-19157	Sequence 19157, A
256	6	0.8	244	7	US-11-188-298-10984	Sequence 10984, A	329	274	6	US-10-506-454-1333	Sequence 1333, Ap
257	6	0.8	245	7	US-11-098-686-11424	Sequence 11424, A	330	275	6	US-10-506-454-159	Sequence 159, App
258	6	0.8	246	7	US-11-051-720-1371	Sequence 1371, Ap	331	276	7	US-11-096-568A-9660	Sequence 9660, Ap
259	6	0.8	246	7	US-11-051-720-1442	Sequence 1442, Ap	332	278	7	US-11-079-463-9219	Sequence 9219, Ap
260	6	0.8	246	7	US-11-096-568A-7431	Sequence 7431, Ap	333	280	7	US-11-079-463-7570	Sequence 7570, Ap
261	6	0.8	247	7	US-11-054-515-1384	Sequence 1384, Ap	334	281	6	US-11-096-568A-33368	Sequence 33368, A
262	6	0.8	247	7	US-11-266-444-1384	Sequence 1384, Ap	335	282	7	US-11-096-568A-15872	Sequence 15872, A
263	6	0.8	248	7	US-11-087-099-5851	Sequence 5851, Ap	336	283	6	US-10-506-454-1410	Sequence 1410, Ap
264	6	0.8	248	7	US-11-087-099-5851	Sequence 5851, Ap	337	283	7	US-11-096-568A-13650	Sequence 13650, A
265	6	0.8	249	7	US-11-087-099-5851	Sequence 5851, Ap	338	284	6	US-11-096-568A-27955	Sequence 27955, A
266	6	0.8	249	7	US-11-096-568A-24893	Sequence 24893, A	339	284	7	US-11-096-568A-17484	Sequence 17484, A
267	6	0.8	250	7	US-11-096-568A-21531	Sequence 21531, A	340	284	7	US-11-096-568A-31905	Sequence 31905, A
268	6	0.8	251	7	US-11-096-568A-692	Sequence 692, App	341	286	6	US-10-467-657-1254	Sequence 1254, Ap
269	6	0.8	251	7	US-11-096-568A-1254	Sequence 1254, Ap	342	287	7	US-11-087-099-9350	Sequence 9350, Ap
270	6	0.8	251	7	US-11-096-568A-22969	Sequence 22969, A	343	287	7	US-11-096-568A-1253	Sequence 1253, Ap
271	6	0.8	251	7	US-11-096-568A-30834	Sequence 30834, A	344	289	7	US-11-096-568A-9987	Sequence 9987, Ap
272	6	0.8	251	7	US-11-188-298-8041	Sequence 8041, Ap	345	289	7	US-11-188-298-11404	Sequence 11404, A
273	6	0.8	252	7	US-11-096-568A-9604	Sequence 9604, Ap	346	291	7	US-11-096-568A-1252	Sequence 1252, Ap
274	6	0.8	252	7	US-11-188-298-2118	Sequence 2118, Ap	347	292	7	US-11-079-463-7825	Sequence 7825, Ap
275	6	0.8	252	7	US-11-188-298-2118	Sequence 2118, Ap	348	293	6	US-10-485-517-203	Sequence 203, App
276	6	0.8	252	7	US-11-188-298-6337	Sequence 6337, Ap	349	293	7	US-11-098-686-10638	Sequence 10638, A
277	6	0.8	252	7	US-11-188-298-9811	Sequence 9811, Ap	350	294	7	US-11-096-568A-18862	Sequence 18862, A
278	6	0.8	252	7	US-11-188-298-10101	Sequence 10101, A	351	294	7	US-11-096-568A-24355	Sequence 24355, A
279	6	0.8	252	7	US-11-188-298-10667	Sequence 10667, A	352	296	7	US-11-096-568A-16867	Sequence 16867, A
280	6	0.8	252	7	US-11-188-298-12269	Sequence 12269, A	353	297	7	US-11-055-822-922	Sequence 922, App
281	6	0.8	252	7	US-11-188-298-20288	Sequence 20288, A	354	297	7	US-11-096-568A-9603	Sequence 9603, Ap
282	6	0.8	253	7	US-11-087-099-6400	Sequence 6400, Ap	355	298	6	US-10-467-657-4362	Sequence 4362, Ap
283	6	0.8	253	7	US-11-188-298-7171	Sequence 7171, Ap	356	299	6	US-10-793-626-1192	Sequence 1192, Ap
284	6	0.8	253	7	US-11-188-298-8654	Sequence 8654, Ap	357	299	6	US-10-467-657-1768	Sequence 1768, Ap
285	6	0.8	253	7	US-11-188-298-10108	Sequence 10108, A	358	299	6	US-10-467-657-4424	Sequence 4424, Ap
286	6	0.8	253	7	US-11-188-298-12998	Sequence 12998, A	359	300	7	US-11-087-099-4351	Sequence 4351, Ap
287	6	0.8	253	7	US-11-188-298-21747	Sequence 21747, A	360	300	7	US-11-079-463-6102	Sequence 6102, Ap
288	6	0.8	254	7	US-11-188-298-8486	Sequence 8486, Ap	361	301	7	US-11-096-568A-18861	Sequence 18861, A
289	6	0.8	254	7	US-11-188-298-17044	Sequence 17044, A	362	301	7	US-11-096-568A-24354	Sequence 24354, A
290	6	0.8	254	7	US-11-188-298-17124	Sequence 17124, A	363	304	6	US-10-934-944-286	Sequence 286, App
291	6	0.8	255	7	US-11-098-686-10492	Sequence 10492, A	364	304	7	US-11-116-881A-295	Sequence 295, App
292	6	0.8	255	7	US-11-188-298-4721	Sequence 4721, Ap	365	304	7	US-11-188-298-4657	Sequence 4657, Ap
293	6	0.8	255	7	US-11-188-298-5790	Sequence 5790, Ap	366	305	7	US-11-096-568A-31765	Sequence 31765, A
294	6	0.8	255	7	US-11-188-298-12957	Sequence 12957, A	367	307	7	US-11-055-822-528	Sequence 528, App
295	6	0.8	255	7	US-11-188-298-14332	Sequence 14332, A	368	308	7	US-11-188-298-12821	Sequence 12821, A
296	6	0.8	255	7	US-11-188-298-16836	Sequence 16836, A	369	309	7	US-11-185-160-2	Sequence 2, Appli
297	6	0.8	255	7	US-11-188-298-17949	Sequence 17949, A	370	310	7	US-11-079-463-5549	Sequence 5549, Ap
298	6	0.8	255	7	US-11-188-298-18645	Sequence 18645, A	371	310	7	US-11-079-463-9722	Sequence 9722, Ap
299	6	0.8	255	7	US-11-188-298-20488	Sequence 20488, A	372	312	7	US-11-172-740-1772	Sequence 1772, Ap
300	6	0.8	256	6	US-10-467-657-6124	Sequence 6124, Ap	373	313	7	US-11-052-554A-316	Sequence 316, App
301	6	0.8	256	7	US-11-096-568A-3389	Sequence 3389, Ap	374	313	7	US-11-156-084-269	Sequence 269, App
302	6	0.8	256	7	US-11-096-568A-22968	Sequence 22968, A	375	313	7	US-11-091-936-3	Sequence 3, Appli
303	6	0.8	256	7	US-11-188-298-2484	Sequence 2484, Ap	376	313	7	US-11-188-298-9309	Sequence 9309, Ap
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305	6	0.8	258	7	US-11-096-568A-5912	Sequence 5912, Ap	378	313	7	US-11-096-568A-8986	Sequence 8986, Ap
306	6	0.8	259	7	US-11-096-568A-28999	Sequence 28999, A	379	314	7	US-11-079-463-7384	Sequence 7384, Ap
307	6	0.8	259	7	US-11-188-298-17925	Sequence 17925, A	380	314	7	US-11-096-568A-8985	Sequence 8985, Ap
308	6	0.8	260	7	US-11-096-568A-31906	Sequence 31906, A	381	316	7	US-11-096-568A-8986	Sequence 8986, Ap
309	6	0.8	260	7	US-11-188-298-10818	Sequence 10818, A	382	316	7	US-11-096-568A-21530	Sequence 21530, A
310	6	0.8	261	7	US-11-000-463-404	Sequence 404, App	383	316	7	US-11-188-298-16788	Sequence 16788, A
311	6	0.8	261	7	US-11-096-568A-15155	Sequence 15155, A	384	317	6	US-10-873-528-65	Sequence 65, Appl
312	6	0.8	261	7	US-11-096-568A-19159	Sequence 19159, A	385	317	7	US-11-096-568A-25604	Sequence 25604, A
313	6	0.8	261	7	US-11-096-568A-22967	Sequence 22967, A	386	317	7	US-11-079-463-8051	Sequence 8051, Ap
314	6	0.8	261	7	US-11-096-568A-25557	Sequence 25557, A	387	318	7	US-11-098-686-11281	Sequence 11281, Ap
315	6	0.8	263	7	US-11-188-298-18423	Sequence 18423, A	388	318	7	US-11-087-099-12185	Sequence 12185, A
316	6	0.8	264	7	US-11-096-568A-15154	Sequence 15154, A	389	318	7	US-11-096-568A-8399	Sequence 8399, Ap
317	6	0.8	264	7	US-11-096-568A-19158	Sequence 19158, A	390	318	7		

391	6	0.8	318	7	US-11-096-568A-23270	Sequence 23270, A	464	6	0.8	345	7	US-11-098-686-10460	Sequence 10460, A
392	6	0.8	320	6	US-10-793-626-2988	Sequence 2988, A	465	6	0.8	345	7	US-11-087-099-1392	Sequence 1292, Ap
393	6	0.8	320	6	US-10-995-561-947	Sequence 947, App	466	6	0.8	345	7	US-11-188-298-6310	Sequence 6310, Ap
394	6	0.8	320	7	US-11-087-099-3546	Sequence 3546, Ap	467	6	0.8	345	7	US-11-188-298-15246	Sequence 15246, A
395	6	0.8	320	7	US-11-096-568A-6440	Sequence 6440, Ap	468	6	0.8	345	7	US-11-188-298-18248	Sequence 18248, A
396	6	0.8	320	7	US-11-096-568A-25656	Sequence 25656, A	469	6	0.8	346	7	US-11-087-099-8092	Sequence 8092, Ap
397	6	0.8	322	7	US-11-079-463-5582	Sequence 5582, Ap	470	6	0.8	347	7	US-11-072-513-2844	Sequence 2844, Ap
398	6	0.8	322	7	US-11-188-298-14564	Sequence 14564, A	471	6	0.8	347	7	US-11-087-099-4236	Sequence 4236, Ap
399	6	0.8	322	7	US-11-188-298-19156	Sequence 19156, A	472	6	0.8	347	7	US-11-096-568A-746	Sequence 746, App
400	6	0.8	324	7	US-11-188-298-22535	Sequence 22535, A	473	6	0.8	347	7	US-11-188-298-3956	Sequence 3956, Ap
401	6	0.8	324	7	US-11-096-568A-23269	Sequence 23269, A	474	6	0.8	347	7	US-11-235-621-5	Sequence 5, Appl1
402	6	0.8	325	7	US-11-072-512-3320	Sequence 3320, Ap	475	6	0.8	348	7	US-11-087-099-7875	Sequence 7875, Ap
403	6	0.8	325	7	US-11-096-568A-23268	Sequence 23268, A	476	6	0.8	348	7	US-11-087-099-9659	Sequence 9659, Ap
404	6	0.8	325	7	US-11-096-568A-31764	Sequence 31764, A	477	6	0.8	348	7	US-11-096-568A-22171	Sequence 22171, A
405	6	0.8	326	7	US-11-087-099-10002	Sequence 10002, A	478	6	0.8	348	7	US-11-188-298-18304	Sequence 18304, A
406	6	0.8	327	7	US-11-096-568A-23939	Sequence 23939, A	479	6	0.8	348	7	US-11-188-298-19437	Sequence 19437, A
407	6	0.8	328	7	US-11-199-233-8	Sequence 8, Appl1	480	6	0.8	348	7	US-11-188-298-19666	Sequence 19666, A
408	6	0.8	329	7	US-11-096-568A-5471	Sequence 5471, Ap	481	6	0.8	348	7	US-11-188-298-21606	Sequence 21606, A
409	6	0.8	329	7	US-11-096-568A-7770	Sequence 7770, Ap	482	6	0.8	349	7	US-11-087-099-11115	Sequence 11115, A
410	6	0.8	329	7	US-11-188-298-13197	Sequence 13197, A	483	6	0.8	349	7	US-11-188-298-705	Sequence 705, App
411	6	0.8	331	7	US-11-079-463-5495	Sequence 5495, Ap	484	6	0.8	349	7	US-11-188-298-8323	Sequence 8323, Ap
412	6	0.8	332	7	US-11-087-099-8851	Sequence 8851, Ap	485	6	0.8	349	7	US-11-188-298-10263	Sequence 10263, A
413	6	0.8	332	7	US-11-096-568A-24353	Sequence 24353, A	486	6	0.8	349	7	US-11-188-298-13758	Sequence 13758, A
414	6	0.8	332	6	US-10-467-657-6974	Sequence 6974, Ap	487	6	0.8	350	7	US-11-096-568A-30833	Sequence 30833, A
415	6	0.8	333	7	US-11-087-099-1297	Sequence 1297, Ap	488	6	0.8	350	7	US-11-188-298-3489	Sequence 3489, Ap
416	6	0.8	333	7	US-11-087-099-6987	Sequence 6987, Ap	489	6	0.8	350	7	US-11-188-298-14066	Sequence 14066, A
417	6	0.8	333	7	US-11-087-099-7269	Sequence 7269, Ap	490	6	0.8	350	7	US-11-188-298-17678	Sequence 17678, A
418	6	0.8	333	7	US-11-087-099-7274	Sequence 7274, Ap	491	6	0.8	350	7	US-11-188-298-22365	Sequence 22365, A
419	6	0.8	333	7	US-11-096-568A-6439	Sequence 6439, Ap	492	6	0.8	351	7	US-11-087-099-8518	Sequence 8518, Ap
420	6	0.8	333	7	US-11-188-298-3343	Sequence 3343, Ap	493	6	0.8	351	7	US-11-087-099-12353	Sequence 12353, A
421	6	0.8	334	7	US-11-087-099-2916	Sequence 2916, Ap	494	6	0.8	351	7	US-11-096-568A-23008	Sequence 23008, A
422	6	0.8	334	7	US-11-087-099-9197	Sequence 9197, Ap	495	6	0.8	351	7	US-11-188-298-6905	Sequence 6905, Ap
423	6	0.8	334	7	US-11-096-568A-12234	Sequence 12234, A	496	6	0.8	352	6	US-10-467-657-984	Sequence 984, App
424	6	0.8	334	7	US-11-188-298-10242	Sequence 10242, A	497	6	0.8	352	7	US-11-087-099-6436	Sequence 6436, Ap
425	6	0.8	335	7	US-11-087-099-5159	Sequence 5159, Ap	498	6	0.8	352	7	US-11-096-568A-31974	Sequence 31974, A
426	6	0.8	336	6	US-10-194-487-182	Sequence 182, App	499	6	0.8	352	7	US-11-188-298-16925	Sequence 16925, A
427	6	0.8	336	6	US-10-195-883-182	Sequence 182, App	500	6	0.8	353	7	US-11-188-298-3584	Sequence 3584, Ap
428	6	0.8	336	6	US-10-195-888-182	Sequence 182, App	501	6	0.8	354	7	US-11-087-099-11419	Sequence 11419, A
429	6	0.8	336	6	US-10-195-889-182	Sequence 182, App	502	6	0.8	355	7	US-11-096-568A-26481	Sequence 26481, A
430	6	0.8	336	6	US-11-087-099-6779	Sequence 6779, Ap	503	6	0.8	355	7	US-11-188-298-7439	Sequence 7439, Ap
431	6	0.8	337	7	US-11-096-568A-33541	Sequence 33541, A	504	6	0.8	356	7	US-11-087-099-3068	Sequence 3068, Ap
432	6	0.8	337	7	US-11-096-568A-13649	Sequence 13649, A	505	6	0.8	356	7	US-11-087-099-12083	Sequence 12083, A
433	6	0.8	338	6	US-10-467-657-8208	Sequence 8208, Ap	506	6	0.8	356	7	US-11-188-298-20200	Sequence 20200, A
434	6	0.8	338	7	US-11-016-564-4	Sequence 4, Appl1	507	6	0.8	357	7	US-11-087-099-11474	Sequence 11474, A
435	6	0.8	338	7	US-11-096-568A-8398	Sequence 8398, Ap	508	6	0.8	357	7	US-11-087-099-13365	Sequence 12365, A
436	6	0.8	338	7	US-11-096-568A-32540	Sequence 32540, A	509	6	0.8	357	7	US-11-096-568A-11144	Sequence 11144, A
437	6	0.8	339	7	US-11-010-239-117	Sequence 117, App	510	6	0.8	358	6	US-10-467-657-1438	Sequence 1438, Ap
438	6	0.8	339	7	US-11-087-099-9109	Sequence 9109, Ap	511	6	0.8	358	6	US-10-525-674-24	Sequence 24, Appl
439	6	0.8	339	7	US-11-096-568A-31793	Sequence 31793, A	512	6	0.8	358	7	US-11-127-877-66	Sequence 66, Appl
440	6	0.8	339	7	US-11-172-740-2504	Sequence 2504, Ap	513	6	0.8	358	7	US-11-087-099-5630	Sequence 5630, Ap
441	6	0.8	339	7	US-10-515-481-3	Sequence 3, Appl1	514	6	0.8	359	7	US-11-096-568A-28150	Sequence 28150, A
442	6	0.8	341	6	US-10-515-481-6	Sequence 6, Appl1	515	6	0.8	360	6	US-10-496-647-10	Sequence 10, Appl
443	6	0.8	341	6	US-10-515-481-9	Sequence 9, Appl1	516	6	0.8	360	6	US-10-496-647-12	Sequence 12, Appl
444	6	0.8	341	6	US-10-515-481-12	Sequence 12, Appl	517	6	0.8	360	6	US-10-496-647-14	Sequence 14, Appl
445	6	0.8	341	6	US-11-087-099-1836	Sequence 1836, Ap	518	6	0.8	360	6	US-10-496-647-16	Sequence 16, Appl
446	6	0.8	341	7	US-11-087-099-4333	Sequence 4333, Ap	519	6	0.8	360	7	US-11-072-512-2211	Sequence 2211, Ap
447	6	0.8	341	7	US-11-087-099-4892	Sequence 4892, Ap	520	6	0.8	361	7	US-11-087-099-2801	Sequence 2801, Ap
448	6	0.8	341	7	US-11-087-099-4892	Sequence 4892, Ap	521	6	0.8	361	7	US-11-096-568A-31792	Sequence 31792, A
449	6	0.8	341	7	US-11-087-099-7320	Sequence 7320, Ap	522	6	0.8	362	7	US-11-087-099-5211	Sequence 5211, Ap
450	6	0.8	341	7	US-11-096-568A-9986	Sequence 9986, Ap	523	6	0.8	362	7	US-11-087-099-6033	Sequence 6033, Ap
451	6	0.8	342	7	US-11-096-568A-15153	Sequence 15153, A	524	6	0.8	362	7	US-11-087-099-9090	Sequence 9090, Ap
452	6	0.8	343	7	US-11-016-564-17	Sequence 17, Appl	525	6	0.8	362	7	US-11-096-568A-6377	Sequence 6377, Ap
453	6	0.8	343	7	US-11-072-512-3068	Sequence 3068, Ap	526	6	0.8	362	7	US-11-096-568A-21529	Sequence 21529, A
454	6	0.8	343	7	US-11-087-099-2134	Sequence 2134, Ap	527	6	0.8	363	6	US-10-878-556A-14	Sequence 14, Appl
455	6	0.8	343	7	US-11-188-298-3028	Sequence 3028, Ap	528	6	0.8	363	7	US-11-098-686-10750	Sequence 10750, A
456	6	0.8	343	7	US-11-188-298-9065	Sequence 9065, Ap	529	6	0.8	363	7	US-11-096-568A-9674	Sequence 9674, Ap
457	6	0.8	343	7	US-11-188-298-10427	Sequence 10427, A	530	6	0.8	364	6	US-10-506-454-1127	Sequence 1127, Ap
458	6	0.8	344	7	US-11-072-512-3358	Sequence 3358, Ap	531	6	0.8	365	7	US-11-096-568A-9673	Sequence 9673, Ap
459	6	0.8	344	7	US-11-087-099-1307	Sequence 1307, Ap	532	6	0.8	366	7	US-11-098-686-11034	Sequence 11034, A
460	6	0.8	344	7	US-11-096-568A-19478	Sequence 19478, A	533	6	0.8	366	7	US-11-087-099-2872	Sequence 2872, Ap
461	6	0.8	344	7	US-11-079-463-8052	Sequence 8052, Ap	534	6	0.8	366	7	US-11-087-099-4133	Sequence 4133, Ap
462	6	0.8	344	7	US-11-188-298-3060	Sequence 3060, Ap	535	6	0.8	366	7	US-11-087-099-4201	Sequence 4201, Ap
463	6	0.8	344	7	US-11-188-298-17164	Sequence 17164, A	536	6	0.8	366	7	US-11-087-099-7455	Sequence 7455, Ap

537	6	0.8	366	7	US-11-087-099-9353	Sequence 9353, Ap	610	384	7	US-11-096-568A-8950	Sequence 8950, Ap
538	6	0.8	366	7	US-11-087-099-12100	Sequence 12100, A	611	384	7	US-11-096-568A-13022	Sequence 13022, A
539	6	0.8	366	7	US-11-096-568A-745	Sequence 745, App	612	385	6	US-10-995-561-945	Sequence 945, App
540	6	0.8	366	7	US-11-096-568A-31973	Sequence 31973, A	613	385	6	US-10-995-561-949	Sequence 949, App
541	6	0.8	367	7	US-11-152-366-35	Sequence 35, Appl	614	385	7	US-11-087-099-7112	Sequence 7112, Ap
542	6	0.8	368	6	US-10-858-730-217	Sequence 217, App	615	385	7	US-11-096-568A-23006	Sequence 23006, A
543	6	0.8	368	6	US-10-501-035-249	Sequence 249, App	616	386	7	US-11-087-099-11460	Sequence 11460, A
544	6	0.8	368	6	US-11-087-099-936	Sequence 936, App	617	387	7	US-11-096-568A-25143	Sequence 25143, A
545	6	0.8	368	7	US-11-087-099-4522	Sequence 4522, Ap	618	387	7	US-11-188-298-3125	Sequence 3125, Ap
546	6	0.8	368	7	US-11-087-099-9713	Sequence 9713, Ap	619	387	7	US-11-235-621-15	Sequence 15, Appl
547	6	0.8	368	7	US-11-087-099-11484	Sequence 11484, A	620	388	7	US-11-096-568A-15902	Sequence 15902, A
548	6	0.8	368	7	US-11-087-099-11862	Sequence 11862, A	621	388	7	US-11-188-298-19057	Sequence 19057, A
549	6	0.8	369	7	US-11-087-099-2275	Sequence 2275, Ap	622	389	7	US-11-087-099-7218	Sequence 7218, Ap
550	6	0.8	369	7	US-11-188-298-10395	Sequence 10395, A	623	389	7	US-11-096-568A-25142	Sequence 25142, A
551	6	0.8	370	7	US-11-087-099-5213	Sequence 5213, Ap	624	390	7	US-11-188-298-21687	Sequence 21687, A
552	6	0.8	370	7	US-11-087-099-6710	Sequence 6710, Ap	625	391	7	US-11-087-099-9851	Sequence 9851, Ap
553	6	0.8	370	7	US-11-087-099-8655	Sequence 8655, Ap	626	392	6	US-10-793-626-2494	Sequence 2494, Ap
554	6	0.8	370	7	US-11-087-099-10826	Sequence 10826, A	627	392	6	US-11-188-298-4450	Sequence 4450, Ap
555	6	0.8	370	7	US-11-087-099-11201	Sequence 11201, A	628	393	7	US-11-096-568A-34047	Sequence 34047, A
556	6	0.8	370	7	US-11-096-568A-12233	Sequence 12233, A	629	393	7	US-11-087-099-6327	Sequence 6327, Ap
557	6	0.8	370	7	US-11-188-298-6124	Sequence 6124, Ap	630	394	7	US-11-188-298-18746	Sequence 18746, A
558	6	0.8	370	7	US-11-188-298-9992	Sequence 9992, Ap	631	394	7	US-09-978-360A-769	Sequence 769, App
559	6	0.8	371	7	US-11-096-568A-26480	Sequence 26480, A	632	395	6	US-10-858-730-218	Sequence 218, App
560	6	0.8	371	7	US-11-096-568A-31791	Sequence 31791, A	633	395	6	US-10-467-657-4484	Sequence 4484, Ap
561	6	0.8	372	6	US-10-844-035-1	Sequence 1, Appl	634	395	7	US-11-072-175-235	Sequence 235, App
562	6	0.8	372	7	US-11-188-298-5057	Sequence 5057, Ap	635	396	7	US-11-188-298-3141	Sequence 3141, Ap
563	6	0.8	372	7	US-11-188-298-22470	Sequence 22470, A	636	396	7	US-11-120-543-10	Sequence 10, Appl
564	6	0.8	373	6	US-10-995-561-948	Sequence 948, App	637	396	7	US-11-096-568A-11143	Sequence 11143, A
565	6	0.8	373	7	US-11-082-389-200	Sequence 200, App	638	396	7	US-11-079-463-7583	Sequence 7583, Ap
566	6	0.8	373	7	US-11-087-099-8055	Sequence 8055, Ap	639	397	7	US-11-188-298-8578	Sequence 8578, Ap
567	6	0.8	373	7	US-11-096-568A-28149	Sequence 28149, A	640	397	7	US-11-216-267-34	Sequence 34, Appl
568	6	0.8	373	7	US-11-188-298-10929	Sequence 10929, A	641	397	7	US-11-232-382-34	Sequence 23, Appl
569	6	0.8	373	7	US-11-188-298-21280	Sequence 21280, A	642	398	6	US-10-517-939-210	Sequence 210, App
570	6	0.8	374	6	US-10-793-626-1356	Sequence 1356, Ap	643	398	7	US-11-096-568A-10967	Sequence 10967, A
571	6	0.8	374	7	US-11-096-568A-25555	Sequence 25555, A	644	398	7	US-11-096-568A-9672	Sequence 9672, Ap
572	6	0.8	374	7	US-11-079-463-9216	Sequence 9216, Ap	645	398	7	US-11-096-568A-9985	Sequence 9985, Ap
573	6	0.8	374	7	US-11-188-298-895	Sequence 895, App	646	398	7	US-11-188-298-1239	Sequence 1239, Ap
574	6	0.8	374	7	US-11-188-298-3309	Sequence 3309, Ap	647	399	6	US-10-650-326B-23	Sequence 23, Appl
575	6	0.8	374	7	US-11-188-298-3366	Sequence 3366, Ap	648	399	7	US-11-051-568-27	Sequence 27, Appl
576	6	0.8	374	7	US-11-188-298-10019	Sequence 10019, A	649	399	7	US-11-226-555-23	Sequence 23, Appl
577	6	0.8	374	7	US-11-188-298-12373	Sequence 12373, A	650	399	7	US-11-096-568A-26912	Sequence 26912, A
578	6	0.8	375	6	US-10-995-561-946	Sequence 946, App	651	399	7	US-11-096-568A-29398	Sequence 29398, A
579	6	0.8	375	7	US-11-096-568A-26913	Sequence 26913, A	652	399	7	US-11-096-568A-31593	Sequence 31593, A
580	6	0.8	375	7	US-11-188-298-17154	Sequence 17154, A	653	399	7	US-11-096-568A-34046	Sequence 34046, A
581	6	0.8	375	7	US-11-188-298-22159	Sequence 22159, A	654	400	7	US-11-120-543-12	Sequence 12, Appl
582	6	0.8	376	6	US-10-501-035-289	Sequence 289, App	655	400	7	US-11-096-568A-27568	Sequence 27568, A
583	6	0.8	376	7	US-11-169-041-143	Sequence 143, App	656	401	7	US-11-096-568A-31592	Sequence 31592, A
584	6	0.8	376	7	US-11-096-568A-27954	Sequence 27954, A	657	402	7	US-11-188-298-2264	Sequence 2264, Ap
585	6	0.8	376	7	US-11-188-298-717	Sequence 717, App	658	403	7	US-11-188-298-2750	Sequence 2750, Ap
586	6	0.8	377	7	US-11-096-568A-23007	Sequence 23007, A	659	403	7	US-11-188-298-13830	Sequence 13830, A
587	6	0.8	377	7	US-11-079-463-6182	Sequence 6182, Ap	660	404	7	US-11-188-298-14787	Sequence 14787, A
588	6	0.8	377	7	US-11-188-298-7208	Sequence 7208, Ap	661	404	7	US-11-188-298-661	Sequence 661, App
589	6	0.8	379	6	US-10-131-826A-328	Sequence 328, App	662	405	7	US-11-087-099-6553	Sequence 6553, Ap
590	6	0.8	379	6	US-10-858-730-22	Sequence 22, Appl	663	405	7	US-11-087-099-6553	Sequence 11442, A
591	6	0.8	379	6	US-10-525-674-6	Sequence 6, Appl	664	405	7	US-11-096-568A-11142	Sequence 13339, A
592	6	0.8	379	6	US-11-073-115B-328	Sequence 328, App	665	406	7	US-11-096-568A-10009	Sequence 10009, A
593	6	0.8	379	7	US-11-087-099-5645	Sequence 5645, Ap	666	407	7	US-11-087-099-3465	Sequence 3465, Ap
594	6	0.8	379	7	US-11-087-099-11045	Sequence 11045, A	667	408	7	US-11-087-099-5495	Sequence 5495, Ap
595	6	0.8	379	7	US-11-096-568A-10010	Sequence 10010, A	668	408	7	US-11-087-099-9556	Sequence 9556, Ap
596	6	0.8	379	7	US-11-290-153-328	Sequence 328, App	669	409	6	US-10-878-556A-55	Sequence 55, Appl
597	6	0.8	380	7	US-11-144-833-12	Sequence 12, Appl	670	409	7	US-11-219-282-33	Sequence 33, Appl
598	6	0.8	380	7	US-11-144-833-13	Sequence 13, Appl	671	409	7	US-11-096-568A-28976	Sequence 28976, A
599	6	0.8	381	7	US-11-087-099-4409	Sequence 4409, Ap	672	410	6	US-10-467-657-4864	Sequence 4864, Ap
600	6	0.8	382	7	US-11-087-099-820	Sequence 820, App	673	410	7	US-11-096-568A-28998	Sequence 28998, A
601	6	0.8	382	7	US-11-096-568A-6376	Sequence 6376, Ap	674	410	7	US-11-096-568A-28998	Sequence 12597, A
602	6	0.8	383	7	US-11-096-568A-9897	Sequence 9897, Ap	675	410	7	US-11-188-298-21597	Sequence 21597, A
603	6	0.8	384	7	US-11-120-543-2	Sequence 2, Appl	676	411	7	US-11-096-568A-29397	Sequence 29397, A
604	6	0.8	384	7	US-11-120-543-6	Sequence 6, Appl	677	412	7	US-11-096-568A-18897	Sequence 18897, A
605	6	0.8	384	7	US-11-120-543-6	Sequence 6, Appl	678	412	7	US-11-188-298-5342	Sequence 5342, Ap
606	6	0.8	384	7	US-11-120-543-8	Sequence 8, Appl	679	413	7	US-11-188-298-5513	Sequence 5513, Ap
607	6	0.8	384	7	US-11-120-543-14	Sequence 14, Appl	680	413	7	US-11-096-568A-13021	Sequence 13021, A
608	6	0.8	384	7	US-11-120-543-22	Sequence 22, Appl	681	415	7	US-11-096-568A-8947	Sequence 8947, Ap
609	6	0.8	384	7	US-11-096-568A-8948	Sequence 8948, Ap	682	415	7	US-11-096-568A-28148	Sequence 28148, A

683	6	0.8	417	7	US-11-096-568A-8397	Sequence 8397, Ap	756	6	0.8	463	7	US-11-087-099-2195	Sequence 2195, Ap
684	6	0.8	417	7	US-11-096-568A-28118	Sequence 28118, A	757	6	0.8	463	7	US-11-087-099-6438	Sequence 6438, Ap
685	6	0.8	418	7	US-11-086-284-187	Sequence 187, App	758	6	0.8	464	7	US-11-087-099-2868	Sequence 2868, Ap
686	6	0.8	419	7	US-11-096-568A-26911	Sequence 26911, A	759	6	0.8	464	7	US-11-087-099-4303	Sequence 4303, Ap
687	6	0.8	420	6	US-10-520-543-16	Sequence 14, Appl	760	6	0.8	464	7	US-11-087-099-6109	Sequence 6109, Ap
688	6	0.8	421	7	US-11-120-543-14	Sequence 16, Appl	761	6	0.8	464	7	US-11-188-298-14990	Sequence 14990, A
689	6	0.8	422	7	US-11-120-543-20	Sequence 20, Appl	762	6	0.8	464	7	US-11-188-298-16612	Sequence 16612, A
690	6	0.8	424	6	US-10-467-657-90	Sequence 90, Appl	763	6	0.8	467	7	US-11-188-298-17127	Sequence 17127, A
691	6	0.8	424	6	US-10-467-657-6344	Sequence 6344, Ap	764	6	0.8	469	7	US-11-072-512-2219	Sequence 2219, Ap
692	6	0.8	424	7	US-11-096-568A-19820	Sequence 19820, A	765	6	0.8	471	7	US-11-188-298-3821	Sequence 3821, Ap
693	6	0.8	427	7	US-11-188-298-7493	Sequence 7493, Ap	766	6	0.8	473	6	US-10-934-944-376	Sequence 376, App
694	6	0.8	428	7	US-11-096-568A-19819	Sequence 19819, A	767	6	0.8	473	6	US-10-934-944-381	Sequence 381, App
695	6	0.8	428	7	US-11-096-568A-31591	Sequence 31591, A	768	6	0.8	473	6	US-10-934-944-382	Sequence 382, App
696	6	0.8	428	7	US-11-188-298-19822	Sequence 19822, A	769	6	0.8	473	7	US-11-087-099-8304	Sequence 8304, Ap
697	6	0.8	429	7	US-11-188-298-5490	Sequence 5490, Ap	770	6	0.8	473	7	US-11-116-881A-2272	Sequence 2272, Ap
698	6	0.8	429	7	US-11-188-298-19897	Sequence 19897, A	771	6	0.8	473	7	US-11-116-881A-2278	Sequence 2278, Ap
699	6	0.8	430	7	US-11-172-740-330	Sequence 330, App	772	6	0.8	473	7	US-11-116-881A-2300	Sequence 2300, Ap
700	6	0.8	430	7	US-11-172-740-331	Sequence 331, App	773	6	0.8	473	7	US-11-188-298-1307	Sequence 1307, Ap
701	6	0.8	430	7	US-11-188-298-3502	Sequence 3502, Ap	774	6	0.8	473	7	US-11-188-298-2143	Sequence 2143, Ap
702	6	0.8	430	7	US-11-188-298-14611	Sequence 14611, A	775	6	0.8	473	7	US-11-188-298-4129	Sequence 4129, Ap
703	6	0.8	431	6	US-10-525-674-26	Sequence 26, Appl	776	6	0.8	473	7	US-11-188-298-4172	Sequence 4172, Ap
704	6	0.8	431	7	US-11-188-298-5792	Sequence 5792, Ap	777	6	0.8	473	7	US-11-188-298-12250	Sequence 12250, A
705	6	0.8	431	7	US-11-188-298-9889	Sequence 9889, Ap	778	6	0.8	473	7	US-11-188-298-13095	Sequence 13095, A
706	6	0.8	431	7	US-11-188-298-12175	Sequence 12175, A	779	6	0.8	473	7	US-11-188-298-18298	Sequence 18298, A
707	6	0.8	431	7	US-11-188-298-13508	Sequence 13508, A	780	6	0.8	474	7	US-11-188-298-667	Sequence 667, App
708	6	0.8	432	7	US-11-087-099-704	Sequence 704, App	781	6	0.8	474	7	US-11-188-298-5955	Sequence 5955, Ap
709	6	0.8	432	7	US-11-087-099-10706	Sequence 10706, A	782	6	0.8	474	7	US-11-188-298-14126	Sequence 14126, A
710	6	0.8	432	7	US-11-096-568A-25141	Sequence 25141, A	783	6	0.8	474	7	US-11-188-298-2242	Sequence 2242, A
711	6	0.8	432	7	US-11-188-298-19037	Sequence 19037, A	784	6	0.8	474	7	US-11-188-298-22303	Sequence 22303, A
712	6	0.8	434	7	US-11-196-475-164	Sequence 164, App	785	6	0.8	475	6	US-10-510-386-98	Sequence 98, Appl
713	6	0.8	436	7	US-11-087-099-11529	Sequence 11529, A	786	6	0.8	475	7	US-11-087-099-2709	Sequence 2709, Ap
714	6	0.8	436	7	US-11-188-298-22548	Sequence 22548, A	787	6	0.8	475	7	US-11-188-298-2476	Sequence 2476, Ap
715	6	0.8	437	7	US-11-073-626-1	Sequence 1, Appl	788	6	0.8	475	7	US-11-188-298-2585	Sequence 2585, Ap
716	6	0.8	437	7	US-11-087-099-3654	Sequence 3654, Ap	789	6	0.8	476	7	US-11-188-298-15793	Sequence 15793, A
717	6	0.8	437	7	US-11-188-298-19155	Sequence 19155, A	790	6	0.8	476	7	US-11-188-298-18547	Sequence 18547, A
718	6	0.8	438	7	US-11-096-568A-30832	Sequence 30832, A	791	6	0.8	477	7	US-11-087-099-8801	Sequence 8801, Ap
719	6	0.8	439	7	US-11-079-463-6330	Sequence 6330, Ap	792	6	0.8	479	7	US-11-096-568A-19818	Sequence 19818, Ap
720	6	0.8	439	7	US-11-079-463-8028	Sequence 8028, Ap	793	6	0.8	479	7	US-11-096-568A-28975	Sequence 28975, A
721	6	0.8	439	7	US-11-188-298-3673	Sequence 3673, Ap	794	6	0.8	479	7	US-11-188-298-12225	Sequence 12225, A
722	6	0.8	440	7	US-11-072-512-3856	Sequence 3856, Ap	795	6	0.8	480	7	US-11-096-568A-26612	Sequence 26612, A
723	6	0.8	440	7	US-11-188-298-10114	Sequence 10114, A	796	6	0.8	482	7	US-11-055-822-20	Sequence 20, Appl
724	6	0.8	442	6	US-10-513-639-25	Sequence 25, Appl	797	6	0.8	482	7	US-11-096-568A-9895	Sequence 9895, Ap
725	6	0.8	442	6	US-10-506-454-1590	Sequence 1590, Ap	798	6	0.8	482	7	US-11-096-568A-12959	Sequence 12959, A
726	6	0.8	443	7	US-11-051-720-1734	Sequence 1734, Ap	799	6	0.8	482	7	US-11-188-298-6868	Sequence 6868, Ap
727	6	0.8	444	6	US-10-467-657-2414	Sequence 2414, Ap	800	6	0.8	483	7	US-11-087-099-9313	Sequence 9313, Ap
728	6	0.8	445	7	US-11-074-176-182	Sequence 182, App	801	6	0.8	483	7	US-11-096-568A-18833	Sequence 18833, A
729	6	0.8	446	7	US-11-188-298-3929	Sequence 3929, Ap	802	6	0.8	483	7	US-11-188-298-19672	Sequence 19672, A
730	6	0.8	447	7	US-11-096-568A-26613	Sequence 26613, A	803	6	0.8	484	7	US-11-188-298-13873	Sequence 13873, A
731	6	0.8	447	7	US-11-096-568A-28117	Sequence 28117, A	804	6	0.8	485	6	US-10-501-035-349	Sequence 349, App
732	6	0.8	448	7	US-11-188-298-11427	Sequence 11427, A	805	6	0.8	485	7	US-11-055-822-18	Sequence 18, Appl
733	6	0.8	449	7	US-11-087-099-11350	Sequence 11350, A	806	6	0.8	486	7	US-11-087-099-9830	Sequence 9830, Ap
734	6	0.8	450	7	US-11-188-298-336	Sequence 336, App	807	6	0.8	486	7	US-11-079-463-8878	Sequence 8878, Ap
735	6	0.8	450	7	US-11-188-298-12480	Sequence 12480, A	808	6	0.8	486	7	US-11-188-298-11517	Sequence 11517, A
736	6	0.8	451	7	US-11-087-099-1581	Sequence 1581, Ap	809	6	0.8	486	7	US-11-188-298-17433	Sequence 17433, A
737	6	0.8	451	7	US-11-096-568A-9896	Sequence 9896, Ap	810	6	0.8	486	7	US-11-188-298-21031	Sequence 21031, A
738	6	0.8	452	7	US-11-188-298-9746	Sequence 9746, Ap	811	6	0.8	486	7	US-11-188-298-21597	Sequence 21597, A
739	6	0.8	453	6	US-10-467-657-1642	Sequence 1642, Ap	812	6	0.8	487	7	US-11-087-099-3264	Sequence 3264, Ap
740	6	0.8	453	7	US-11-096-568A-27953	Sequence 27953, A	813	6	0.8	487	7	US-11-188-298-6934	Sequence 6934, Ap
741	6	0.8	453	7	US-11-188-298-13421	Sequence 13421, A	814	6	0.8	487	7	US-11-188-298-13142	Sequence 13142, A
742	6	0.8	453	7	US-11-188-298-20441	Sequence 20441, A	815	6	0.8	488	7	US-11-188-298-8600	Sequence 8600, Ap
743	6	0.8	454	7	US-11-087-099-12184	Sequence 12184, A	816	6	0.8	488	7	US-11-188-298-9657	Sequence 9657, Ap
744	6	0.8	455	7	US-11-087-099-8847	Sequence 8847, Ap	817	6	0.8	489	7	US-11-188-298-8600	Sequence 8600, Ap
745	6	0.8	456	7	US-11-098-686-11117	Sequence 11117, A	818	6	0.8	490	7	US-11-096-568A-31601	Sequence 31601, A
746	6	0.8	457	7	US-11-246-793-2	Sequence 2, Appl	819	6	0.8	490	7	US-11-188-298-3993	Sequence 3993, Ap
747	6	0.8	457	7	US-11-246-793-48	Sequence 48, Appl	820	6	0.8	490	7	US-11-188-298-6814	Sequence 6814, Ap
748	6	0.8	457	7	US-11-246-793-50	Sequence 50, Appl	821	6	0.8	490	7	US-11-188-298-9922	Sequence 9922, Ap
749	6	0.8	458	6	US-10-454-437-340	Sequence 340, App	822	6	0.8	491	7	US-11-205-109-21	Sequence 21, Appl
750	6	0.8	459	7	US-11-188-298-19083	Sequence 19083, A	823	6	0.8	491	7	US-11-087-099-11095	Sequence 11095, A
751	6	0.8	461	6	US-10-934-944-176	Sequence 176, App	824	6	0.8	493	7	US-11-188-298-7250	Sequence 7250, Ap
752	6	0.8	461	7	US-11-116-881A-185	Sequence 185, App	825	6	0.8	495	6	US-10-467-9628-93	Sequence 93, Appl
753	6	0.8	462	7	US-11-087-099-2409	Sequence 2409, Ap	826	6	0.8	495	7	US-11-087-099-3528	Sequence 3528, Ap
754	6	0.8	463	7	US-11-128-900-4	Sequence 4, Appl	827	6	0.8	495	7	US-11-087-099-11944	Sequence 11944, A
755	6	0.8	463	7	US-11-128-900-68	Sequence 68, Appl	828	6	0.8	495	7	US-11-188-298-22312	Sequence 22312, A

829	6	0.8	496	7	US-11-096-568A-31600	Sequence 31600, A	902	6	0.8	549	7	US-11-188-298-5783	Sequence 5783, Ap
830	6	0.8	496	7	US-11-079-463-9399	Sequence 9399, Ap	903	6	0.8	551	7	US-11-079-463-8767	Sequence 8767, Ap
831	6	0.8	498	7	US-11-188-298-8378	Sequence 8378, Ap	904	6	0.8	554	7	US-11-188-298-2588	Sequence 2588, Ap
832	6	0.8	498	7	US-11-188-298-16314	Sequence 16314, A	905	6	0.8	555	7	US-11-188-298-20131	Sequence 20131, A
833	6	0.8	498	7	US-11-188-298-20979	Sequence 20979, A	906	6	0.8	555	7	US-11-188-298-22563	Sequence 22563, A
834	6	0.8	499	7	US-11-188-298-6962	Sequence 6962, Ap	907	6	0.8	556	6	US-10-467-657-498	Sequence 498, App
835	6	0.8	500	7	US-11-087-099-9861	Sequence 9861, Ap	908	6	0.8	556	6	US-10-467-657-498	Sequence 498, App
836	6	0.8	500	7	US-11-087-099-12411	Sequence 12411, A	909	6	0.8	557	6	US-11-188-298-20449	Sequence 20449, A
837	6	0.8	500	7	US-11-096-568A-18410	Sequence 18410, A	910	6	0.8	557	6	US-10-467-657-2888	Sequence 2888, Ap
838	6	0.8	500	7	US-11-096-568A-32877	Sequence 32877, A	911	6	0.8	558	7	US-11-096-568A-34045	Sequence 34045, A
839	6	0.8	502	7	US-11-199-233-13	Sequence 13, Appl	912	6	0.8	559	7	US-11-188-298-986	Sequence 986, App
840	6	0.8	503	7	US-11-082-389-290	Sequence 290, App	913	6	0.8	560	7	US-11-096-568A-18831	Sequence 18831, A
841	6	0.8	504	6	US-10-934-944-178	Sequence 178, App	914	6	0.8	562	6	US-10-506-454-1289	Sequence 1289, Ap
842	6	0.8	504	7	US-11-116-881A-187	Sequence 187, App	915	6	0.8	562	7	US-11-096-568A-30550	Sequence 30550, A
843	6	0.8	505	6	US-10-763-712A-26	Sequence 26, Appl	916	6	0.8	563	7	US-11-055-822-254	Sequence 254, App
844	6	0.8	505	6	US-10-763-712A-88	Sequence 88, Appl	917	6	0.8	565	7	US-11-087-099-3971	Sequence 3971, Ap
845	6	0.8	505	6	US-10-763-712A-89	Sequence 89, Appl	918	6	0.8	565	7	US-11-072-512-3772	Sequence 3772, Ap
846	6	0.8	505	6	US-10-763-712A-123	Sequence 123, App	919	6	0.8	567	7	US-11-188-298-929	Sequence 929, App
847	6	0.8	505	7	US-11-079-463-8719	Sequence 8719, Ap	920	6	0.8	567	7	US-11-188-298-929	Sequence 929, App
848	6	0.8	506	6	US-10-873-528-80	Sequence 80, Appl	921	6	0.8	568	7	US-11-185-342-15	Sequence 15, Appl
849	6	0.8	506	7	US-11-087-099-10758	Sequence 10758, A	922	6	0.8	568	7	US-11-188-298-2752	Sequence 2752, Ap
850	6	0.8	506	7	US-11-096-568A-34051	Sequence 34051, A	923	6	0.8	568	7	US-11-188-298-4524	Sequence 4524, Ap
851	6	0.8	507	7	US-11-096-568A-18409	Sequence 18409, A	924	6	0.8	568	7	US-11-188-298-14329	Sequence 14329, A
852	6	0.8	507	7	US-11-096-568A-32876	Sequence 32876, A	925	6	0.8	568	7	US-11-188-298-22054	Sequence 22054, A
853	6	0.8	507	7	US-11-188-298-11793	Sequence 11793, A	926	6	0.8	572	7	US-11-096-568A-12957	Sequence 12957, A
854	6	0.8	509	6	US-10-793-626-98	Sequence 98, Appl	927	6	0.8	573	7	US-11-188-298-14241	Sequence 14241, A
855	6	0.8	510	7	US-11-087-099-1859	Sequence 1859, Ap	928	6	0.8	574	6	US-10-517-939-108	Sequence 108, App
856	6	0.8	510	7	US-11-188-298-12808	Sequence 12808, A	929	6	0.8	575	7	US-11-188-298-1157	Sequence 1157, Ap
857	6	0.8	511	7	US-11-087-099-7567	Sequence 7567, Ap	930	6	0.8	575	7	US-11-188-298-3182	Sequence 3182, Ap
858	6	0.8	511	7	US-11-188-298-17979	Sequence 17979, A	931	6	0.8	576	7	US-11-096-568A-8957	Sequence 8957, Ap
859	6	0.8	511	7	US-11-188-298-19503	Sequence 19503, A	932	6	0.8	576	7	US-11-096-568A-8959	Sequence 8959, Ap
860	6	0.8	512	7	US-11-087-099-5209	Sequence 5209, Ap	933	6	0.8	583	7	US-11-079-463-9397	Sequence 9397, Ap
861	6	0.8	512	7	US-11-188-298-4771	Sequence 4771, Ap	934	6	0.8	585	7	US-11-188-298-6205	Sequence 6205, Ap
862	6	0.8	513	6	US-10-934-944-272	Sequence 272, App	935	6	0.8	587	7	US-11-087-099-11657	Sequence 11657, A
863	6	0.8	513	7	US-11-135-667-63	Sequence 63, Appl	936	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
864	6	0.8	513	7	US-11-116-881A-281	Sequence 281, App	937	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
865	6	0.8	514	7	US-11-235-621-17	Sequence 17, Appl	938	6	0.8	587	7	US-11-079-463-8026	Sequence 8026, Ap
866	6	0.8	515	7	US-11-087-099-4968	Sequence 4968, Ap	939	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
867	6	0.8	517	7	US-11-188-298-19638	Sequence 19638, A	940	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
868	6	0.8	518	6	US-10-934-944-298	Sequence 298, App	941	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
869	6	0.8	518	7	US-11-116-881A-307	Sequence 307, App	942	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
870	6	0.8	519	6	US-10-485-517-220	Sequence 220, App	943	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
871	6	0.8	519	6	US-11-188-298-4344	Sequence 4344, A	944	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
872	6	0.8	519	7	US-11-188-298-4344	Sequence 4344, A	945	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
873	6	0.8	519	7	US-11-188-298-21708	Sequence 21708, A	946	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
874	6	0.8	520	7	US-11-188-298-4143	Sequence 4143, Ap	947	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
875	6	0.8	521	7	US-11-096-568A-26611	Sequence 26611, A	948	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
876	6	0.8	521	7	US-11-096-568A-34050	Sequence 34050, A	949	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
877	6	0.8	521	7	US-11-096-568A-18408	Sequence 18408, A	950	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
878	6	0.8	522	7	US-11-096-568A-32875	Sequence 32875, A	951	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
879	6	0.8	522	7	US-11-087-099-7839	Sequence 7839, Ap	952	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
880	6	0.8	529	7	US-11-087-099-1839	Sequence 1839, Ap	953	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
881	6	0.8	530	7	US-11-096-568A-15792	Sequence 15792, A	954	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
882	6	0.8	530	7	US-11-096-568A-28974	Sequence 28974, A	955	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
883	6	0.8	532	7	US-11-087-099-12403	Sequence 12403, A	956	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
884	6	0.8	533	7	US-11-087-099-12358	Sequence 12358, A	957	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
885	6	0.8	533	7	US-11-188-298-17096	Sequence 17096, A	958	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
886	6	0.8	534	7	US-11-096-568A-31539	Sequence 31539, A	959	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
887	6	0.8	535	6	US-10-131-826A-124	Sequence 124, App	960	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
888	6	0.8	535	6	US-10-973-115B-124	Sequence 124, App	961	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
889	6	0.8	535	7	US-11-096-568A-18832	Sequence 18832, A	962	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
890	6	0.8	535	7	US-11-290-153-124	Sequence 153, App	963	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
891	6	0.8	537	6	US-10-793-626-1712	Sequence 1712, Ap	964	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
892	6	0.8	537	7	US-11-098-686-10170	Sequence 10170, A	965	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
893	6	0.8	540	7	US-11-188-298-1758	Sequence 1758, Ap	966	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
894	6	0.8	541	7	US-11-096-568A-12958	Sequence 12958, A	967	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
895	6	0.8	542	7	US-11-188-298-1578	Sequence 1578, Ap	968	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
896	6	0.8	545	7	US-11-096-568A-15791	Sequence 15791, A	969	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
897	6	0.8	547	6	US-10-770-726-87	Sequence 87, Appl	970	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
898	6	0.8	547	7	US-11-096-568A-34049	Sequence 34049, A	971	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
899	6	0.8	549	7	US-11-096-070-2	Sequence 2, Appli	972	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
900	6	0.8	549	7	US-11-096-070-6	Sequence 6, Appli	973	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap
901	6	0.8	549	7	US-11-096-070-8	Sequence 8, Appli	974	6	0.8	587	7	US-11-188-298-20209	Sequence 20209, Ap

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975 6 0.8 654 7 US-11-079-463-6150 Sequence 6150, Ap
976 6 0.8 654 7 US-11-188-298-13949 Sequence 13949, A
977 6 0.8 658 7 US-11-079-463-9653 Sequence 9653, Ap
978 6 0.8 658 7 US-11-079-463-9783 Sequence 9783, Ap
979 6 0.8 665 7 US-11-124-368A-289 Sequence 289, App
980 6 0.8 668 6 US-10-467-657-5042 Sequence 5042, Ap
981 6 0.8 668 7 US-11-188-298-1144 Sequence 1144, Ap
982 6 0.8 669 7 US-11-087-099-1120 Sequence 1120, Ap
983 6 0.8 670 7 US-11-188-298-15016 Sequence 15016, A
984 6 0.8 671 6 US-10-506-454-88 Sequence 88, Appl
985 6 0.8 676 7 US-11-098-686-10486 Sequence 10486, A
986 6 0.8 684 7 US-11-188-298-8055 Sequence 8055, Ap
987 6 0.8 687 6 US-10-714-887-268 Sequence 268, App
988 6 0.8 689 7 US-11-079-463-6382 Sequence 6382, Ap
989 6 0.8 692 7 US-11-052-554A-213 Sequence 213, App
990 6 0.8 692 7 US-11-188-298-5840 Sequence 5840, Ap
991 6 0.8 697 7 US-11-052-554A-110 Sequence 110, App
992 6 0.8 698 7 US-11-079-463-6720 Sequence 6720, Ap
993 6 0.8 699 7 US-11-152-601-21 Sequence 21, Appl
994 6 0.8 699 7 US-11-235-621-9 Sequence 9, Appl1
995 6 0.8 700 7 US-11-098-686-10793 Sequence 10793, A
996 6 0.8 701 7 US-11-235-621-1 Sequence 1, Appl1
997 6 0.8 702 7 US-11-188-298-12930 Sequence 12930, A
998 6 0.8 703 7 US-11-079-463-6948 Sequence 6948, Ap
999 6 0.8 703 7 US-11-188-298-16110 Sequence 16110, A
1000 6 0.8 713 7 US-11-188-298-18086 Sequence 18086, A
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ALIGNMENTS

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RESULT 1
US-10-467-657-6026
; Sequence 6026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6026
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6026

Query Match 26.3%; Score 210; DB 6; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.5e-206;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLVATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180

QY 181 FEGNOVYSDRKLRQMSLTGGIWTWLTTRS 210
Db 181 FEGNOVYSDRKLRQMSLTGGIWTWLTTRS 210

;
; ORGANISM: Neisseria gonorrhoeae
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Db 181 FEGNOVYSDRKLRQMSLTGGIWTWLTTRS 210

RESULT 2
US-10-467-657-7528
; Sequence 7528, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 7528
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7528

Query Match 26.3%; Score 210; DB 6; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.5e-206;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLVATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180

QY 181 FEGNOVYSDRKLRQMSLTGGIWTWLTTRS 210
Db 181 FEGNOVYSDRKLRQMSLTGGIWTWLTTRS 210

;
; ORGANISM: Neisseria gonorrhoeae
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RESULT 3
US-11-103-957-92
; Sequence 92, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
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US-11-103-957-92
Query Match      19.7%; Score 157; DB 7; Length 792;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Db 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Qy 392 LGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Db 392 LGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Qy 452 TGKSAALRASRSKTTLNGSLSFDTDPYFTADGVSLGYD 488
Db 452 TGKSAALRASRSKTTLNGSLSFDTDPYFTADGVSLGYD 488

RESULT 4
US-10-506-454-1658
; Sequence 1658, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozayavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; TITLE OF INVENTION: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1658
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
US-10-506-454-1658

Query Match      0.9%; Score 7; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 764 LSPGLPM 770
Db 25 LSPGLPM 31

RESULT 5
US-11-158-655-6
; Sequence 6, Application US/11158655
; Publication No. US20060037089A1
; GENERAL INFORMATION:
; APPLICANT: TSAI, MINDY
; APPLICANT: TAM, SEE-YING
; APPLICANT: GALLI, STEPHEN J
; TITLE OF INVENTION: IN VIVO MODELS FOR RABGEPI- DEPENDENT
; TITLE OF INVENTION: SIGNALING AND FUNCTIONS
; FILE REFERENCE: STAN-371
; CURRENT APPLICATION NUMBER: US/11/158,655
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,755
; PRIOR FILING DATE: 2004-06-24
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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 147
; TYPE: PRT
; ORGANISM: yeast
US-11-158-655-6

Query Match      0.9%; Score 7; DB 7; Length 147;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 416 MSLTERS 422
Db 140 MSLTERS 146

RESULT 6
US-11-087-099-3827
; Sequence 3827, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3827
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Oceanobacillus ihayensis HTE831
US-11-087-099-3827

Query Match      0.9%; Score 7; DB 7; Length 157;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 210 SNQFNEQ 216
Db 63 SNQFNEQ 69

RESULT 7
US-11-172-740-872
; Sequence 872, Application US/11172740
; Publication No. US20060057724A1
; GENERAL INFORMATION:
; APPLICANT: MASCIA, Peter
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: PLANT CHARACTERISTICS AND PHENOTYPES
; FILE REFERENCE: 2750-1602PUS2
; CURRENT APPLICATION NUMBER: US/11/172,740
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,621
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/584,800
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 2523
; SEQ ID NO 872
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(80)
; OTHER INFORMATION: Pfam Name: AP2; Pfam Description: AP2 domain
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION: (17)..(80)
; OTHER INFORMATION: Pfam Name: AP2; Pfam Description: AP2 domain
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for delaying flowering time
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making larger plants
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making plants with increased biomass and foli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Utility: Useful for making smaller plants
; US-11-172-740-872

Query Match          0.9%; Score 7; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 TTTLGSL 471
Db 136 TTTLGSL 142

RESULT 8
US-11-096-568A-1873
; Sequence 1873, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1873
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(222)
; OTHER INFORMATION: Ceres Seq. ID no. 15179541
US-11-096-568A-1873

Query Match          0.9%; Score 7; DB 7; Length 222;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 SATGGRV 735
Db 216 SATGGRV 222

RESULT 9
US-11-096-568A-27201
; Sequence 27201, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27201
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; LENGTH: 222
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(222)
; OTHER INFORMATION: Ceres Seq. ID no. 15179541
US-11-096-568A-27201

Query Match          0.9%; Score 7; DB 7; Length 222;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 SATGGRV 735
Db 216 SATGGRV 222

RESULT 10
US-11-188-298-16796
; Sequence 16796, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 16796
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Pachyaandra terminalis
US-11-188-298-16796

Query Match          0.9%; Score 7; DB 7; Length 238;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 RVEGLQR 35
Db 95 RVEGLQR 101

RESULT 11
US-11-096-568A-1872
; Sequence 1872, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1872
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(241)
; OTHER INFORMATION: Ceres Seq. ID no. 15179540
US-11-096-568A-1872

Query Match          0.9%; Score 7; DB 7; Length 241;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 729 SATGGRV 735
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Db      235 SATGRV 241
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RESULT 12
US-11-096-568A-27200
; Sequence 27200, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 27200
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(241)
; OTHER INFORMATION: Ceres Seq. ID no. 15179540
US-11-096-568A-27200

Query Match      0.9%; Score 7; DB 7; Length 241;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      729 SATGRV 735
|||||
Db      235 SATGRV 241

RESULT 13
US-11-079-463-6578
; Sequence 6578, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bretton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTERIOIDES FRAGILIS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 6578
; LENGTH: 286
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-6578

Query Match      0.9%; Score 7; DB 7; Length 286;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      481 DGVSLGY 487
|||||
Db      110 DGVSLGY 116

RESULT 14
US-11-096-568A-18041
; Sequence 18041, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18041
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(287)
; OTHER INFORMATION: Ceres Seq. ID no. 12362473
US-11-096-568A-18041

Query Match      0.9%; Score 7; DB 7; Length 287;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      451 GTGKSAA 457
|||||
Db      211 GTGKSAA 217

RESULT 15
US-11-188-298-10985
; Sequence 10985, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 10985
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Cicer arietinum
US-11-188-298-10985

Query Match      0.9%; Score 7; DB 7; Length 308;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      324 VOPLPNA 330
|||||
Db      207 VOPLPNA 213

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OM protein - protein search, using sw model

Run on: April 12, 2006, 16:34:33 ; Search time 171 Seconds

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1947.427 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

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Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 1

Total number of hits satisfying chosen parameters: 1864806

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	3	US-09-994-192-4
2	797	100.0	797	5	US-10-606-618-4
3	752	94.4	797	4	US-10-181-660-3
4	752	94.4	797	4	US-10-181-660-11
5	752	94.4	797	4	US-10-320-800-6
6	752	94.4	797	5	US-10-181-600-3
7	752	94.4	797	5	US-10-181-600-11
8	752	94.4	797	5	US-10-988-943-7
9	751	94.2	776	4	US-10-181-660-5
10	751	94.2	776	4	US-10-181-660-13
11	751	94.2	776	5	US-10-181-600-5
12	751	94.2	776	5	US-10-181-600-13
13	210	26.3	792	4	US-10-181-660-7
14	210	26.3	792	5	US-10-181-600-7
15	189	23.7	771	4	US-10-181-660-9
16	189	23.7	771	5	US-10-181-660-9
17	157	19.7	792	3	US-09-994-192-2
18	157	19.7	792	4	US-10-467-534-92
19	157	19.7	792	5	US-10-606-618-2
20	21	2.6	21	4	US-10-181-660-8
21	21	2.6	21	5	US-10-181-660-8
22	19	2.4	21	4	US-10-181-660-4
23	19	2.4	21	5	US-10-181-660-4
24	15	1.9	15	4	US-10-181-660-1
25	15	1.9	15	5	US-10-181-660-1
26	11	1.4	21	4	US-10-181-660-12
27	11	1.4	21	5	US-10-181-660-12

28	9	1.1	177	4	US-10-425-114-63291	Sequence 63291, A
29	9	1.1	246	4	US-10-424-599-149837	Sequence 149837, A
30	9	1.1	381	4	US-10-437-963-154779	Sequence 154779, A
31	9	1.1	408	4	US-10-425-114-72370	Sequence 72370, A
32	9	1.1	408	4	US-10-425-115-266878	Sequence 266878, A
33	9	1.1	443	4	US-10-424-599-14939	Sequence 14939, A
34	9	1.1	1035	4	US-10-389-566-2330	Sequence 2330, A
35	8	1.0	97	3	US-09-933-767-1092	Sequence 1092, A
36	8	1.0	97	4	US-10-004-860-1092	Sequence 1092, A
37	8	1.0	97	4	US-10-023-282-1092	Sequence 168144, A
38	8	1.0	104	4	US-10-437-963-168144	Sequence 217994, A
39	8	1.0	154	4	US-10-424-599-217994	Sequence 4323, A
40	8	1.0	216	4	US-10-369-493-4323	Sequence 51162, A
41	8	1.0	250	4	US-10-425-114-51162	Sequence 46228, A
42	8	1.0	266	5	US-10-450-763-46228	Sequence 4240, A
43	8	1.0	299	3	US-09-738-626-4240	Sequence 13893, A
44	8	1.0	315	4	US-10-369-493-13893	Sequence 146233, A
45	8	1.0	367	4	US-10-437-963-146233	Sequence 14887, A
46	8	1.0	422	5	US-10-369-493-14887	Sequence 48222, A
47	8	1.0	445	5	US-10-450-763-48222	Sequence 13128, A
48	8	1.0	494	4	US-10-369-493-13128	Sequence 479, App
49	8	1.0	583	4	US-10-389-647-479	Sequence 34211, A
50	8	1.0	745	5	US-10-450-763-34211	Sequence 39468, A
51	8	1.0	745	5	US-10-450-763-39468	Sequence 40726, A
52	8	1.0	745	5	US-10-450-763-40726	Sequence 45249, A
53	8	1.0	785	4	US-10-450-763-45249	Sequence 201769, A
54	8	1.0	882	4	US-10-437-963-201769	Sequence 118138, A
55	8	1.0	897	5	US-10-437-963-118138	Sequence 7164, App
56	8	1.0	1577	4	US-10-741-849-7164	Sequence 69069, A
57	8	1.0	2903	5	US-10-282-122A-69069	Sequence 13991, A
58	8	1.0	2903	5	US-10-732-923-13991	Sequence 147, App
59	7	0.9	23	5	US-10-776-224-147	Sequence 275165, A
60	7	0.9	32	4	US-10-425-115-275165	Sequence 352701, A
61	7	0.9	47	4	US-10-425-115-352701	Sequence 40065, A
62	7	0.9	50	3	US-09-864-761-40065	Sequence 25004, A
63	7	0.9	52	4	US-10-425-115-25004	Sequence 341846, A
64	7	0.9	55	4	US-10-767-701-50935	Sequence 10, Appl
65	7	0.9	56	4	US-10-425-115-341846	Sequence 196424, A
66	7	0.9	58	4	US-10-117-604-10	Sequence 144303, A
67	7	0.9	62	4	US-10-425-115-196424	Sequence 203518, A
68	7	0.9	64	4	US-10-424-599-144303	Sequence 53260, A
69	7	0.9	64	4	US-10-424-599-203518	Sequence 248374, A
70	7	0.9	64	4	US-10-767-701-53260	Sequence 190349, A
71	7	0.9	66	4	US-10-424-599-248374	Sequence 359285, A
72	7	0.9	68	4	US-10-424-599-190349	Sequence 249223, A
73	7	0.9	69	4	US-10-425-115-359285	Sequence 43360, A
74	7	0.9	71	4	US-10-424-599-249223	Sequence 246828, A
75	7	0.9	76	4	US-10-282-122A-43360	Sequence 189046, A
76	7	0.9	76	4	US-10-425-115-246828	Sequence 104699, A
77	7	0.9	78	4	US-10-424-599-189046	Sequence 156781, A
78	7	0.9	79	4	US-10-437-963-104699	Sequence 4086, App
79	7	0.9	80	4	US-10-437-963-156781	Sequence 188471, A
80	7	0.9	82	3	US-09-864-408A-4086	Sequence 219581, A
81	7	0.9	83	4	US-10-424-599-188471	Sequence 347, App
82	7	0.9	84	4	US-10-425-115-219581	Sequence 347, App
83	7	0.9	85	4	US-10-369-493-21140	Sequence 325, App
84	7	0.9	87	3	US-09-764-860-347	Sequence 325, App
85	7	0.9	87	4	US-10-074-095-347	Sequence 364770, A
86	7	0.9	87	4	US-10-212-872-347	Sequence 174289, A
87	7	0.9	88	4	US-10-012-542-325	Sequence 188438, A
88	7	0.9	88	4	US-10-115-123-325	Sequence 146654, A
89	7	0.9	88	4	US-10-800-834-325	Sequence 123593, A
90	7	0.9	88	4	US-10-425-115-364770	Sequence 258624, A
91	7	0.9	90	4	US-10-424-599-174289	Sequence 259323, A
92	7	0.9	92	4	US-10-437-963-188438	Sequence 227387, A
93	7	0.9	93	4	US-10-424-599-146654	Sequence 338480, A
94	7	0.9	96	4	US-10-437-963-123593	Sequence 354503, A
95	7	0.9	101	4	US-10-425-115-258624	Sequence 93, Appl
96	7	0.9	102	4	US-10-424-599-259323	
97	7	0.9	105	4	US-10-424-599-227387	
98	7	0.9	106	4	US-10-425-115-338480	
99	7	0.9	107	4	US-10-425-115-354503	
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101	7	0.9	113	4	US-10-425-115-258019	Sequence 258019,	174	7	0.9	310	4	US-10-369-493-12686	Sequence 12686, A
102	7	0.9	122	4	US-10-424-599-166965	Sequence 166965,	175	7	0.9	315	4	US-10-106-698-5557	Sequence 5557, Ap
103	7	0.9	122	4	US-10-424-599-256379	Sequence 256379,	176	7	0.9	324	3	US-09-815-242-13895	Sequence 13895, A
104	7	0.9	122	4	US-10-425-115-347287	Sequence 347287,	177	7	0.9	324	4	US-10-282-122A-76321	Sequence 76321, A
105	7	0.9	122	5	US-10-739-930-8036	Sequence 8036, Ap	178	7	0.9	325	3	US-09-738-626-4841	Sequence 4841, Ap
106	7	0.9	123	4	US-10-425-115-235907	Sequence 235907,	179	7	0.9	325	4	US-10-781-014-776	Sequence 776, App
107	7	0.9	123	4	US-10-425-115-314619	Sequence 314619,	180	7	0.9	327	4	US-10-264-237-1918	Sequence 1918, Ap
108	7	0.9	125	4	US-10-767-701-32380	Sequence 32380, A	181	7	0.9	329	4	US-10-012-819-60	Sequence 60, Appl
109	7	0.9	126	6	US-11-097-143-34038	Sequence 34038, A	182	7	0.9	335	3	US-09-934-455-226	Sequence 226, App
110	7	0.9	129	4	US-10-437-963-104429	Sequence 104429,	183	7	0.9	335	4	US-10-225-066A-834	Sequence 834, App
111	7	0.9	132	4	US-10-476-774-1607	Sequence 1607, Ap	184	7	0.9	335	4	US-10-374-780A-294	Sequence 294, App
112	7	0.9	133	4	US-10-425-115-239682	Sequence 239682,	185	7	0.9	335	5	US-10-225-066A-834	Sequence 834, App
113	7	0.9	145	4	US-10-425-115-368479	Sequence 368479,	186	7	0.9	336	4	US-10-146-733-20	Sequence 20, Appl
114	7	0.9	150	4	US-10-282-122A-54511	Sequence 54511, A	187	7	0.9	337	4	US-10-264-237-2731	Sequence 2731, Ap
115	7	0.9	150	4	US-10-767-701-54531	Sequence 54531, A	188	7	0.9	337	4	US-10-282-122A-74662	Sequence 74662, A
116	7	0.9	150	4	US-10-425-115-187306	Sequence 187306,	189	7	0.9	340	4	US-10-767-701-41329	Sequence 41329, A
117	7	0.9	150	4	US-10-425-115-331739	Sequence 331739,	190	7	0.9	341	5	US-10-450-763-47487	Sequence 47487, A
118	7	0.9	151	4	US-10-424-599-171238	Sequence 171238,	191	7	0.9	341	6	US-11-097-143-21942	Sequence 21942, A
119	7	0.9	154	4	US-10-425-115-331169	Sequence 331169,	192	7	0.9	342	4	US-10-381-898-9	Sequence 9, Appli
120	7	0.9	157	4	US-10-424-599-257335	Sequence 257335,	193	7	0.9	349	4	US-10-282-122A-51887	Sequence 51887, A
121	7	0.9	169	4	US-10-437-963-125771	Sequence 125771,	194	7	0.9	351	4	US-10-369-493-3808	Sequence 3808, Ap
122	7	0.9	171	5	US-10-472-928-2480	Sequence 2480, Ap	195	7	0.9	353	4	US-10-425-115-271431	Sequence 271431
123	7	0.9	176	4	US-10-425-114-49034	Sequence 49034, A	196	7	0.9	355	4	US-10-357-521-4	Sequence 4, Appli
124	7	0.9	176	5	US-10-732-923-5057	Sequence 5057, Ap	197	7	0.9	355	5	US-10-915-029-8	Sequence 8, Appli
125	7	0.9	177	4	US-10-633-680-76	Sequence 76, Appl	198	7	0.9	356	4	US-10-282-122A-52244	Sequence 52244, A
126	7	0.9	177	4	US-10-632-983-55	Sequence 55, Appl	199	7	0.9	359	4	US-10-225-486-54	Sequence 54, Appl
127	7	0.9	178	3	US-09-798-889-76	Sequence 76, Appl	200	7	0.9	366	4	US-10-369-493-1018	Sequence 1018, Ap
128	7	0.9	182	4	US-10-767-701-52318	Sequence 52318, A	201	7	0.9	381	4	US-10-633-680-49	Sequence 49, Appl
129	7	0.9	186	5	US-10-739-930-8997	Sequence 8997, Ap	202	7	0.9	382	3	US-09-798-889-49	Sequence 49, Appl
130	7	0.9	189	5	US-10-450-763-53433	Sequence 53433, A	203	7	0.9	383	3	US-09-738-626-4870	Sequence 4870, Ap
131	7	0.9	191	4	US-10-437-963-133805	Sequence 133805,	204	7	0.9	384	5	US-10-732-923-2861	Sequence 2861, Ap
132	7	0.9	194	4	US-10-424-599-173855	Sequence 173855,	205	7	0.9	386	4	US-10-369-493-8726	Sequence 8726, Ap
133	7	0.9	197	4	US-10-425-114-42546	Sequence 42546, A	206	7	0.9	386	5	US-10-450-763-51472	Sequence 51472, A
134	7	0.9	199	4	US-10-424-599-192625	Sequence 192625,	207	7	0.9	390	4	US-10-282-122A-48185	Sequence 48185, A
135	7	0.9	199	4	US-10-767-701-46512	Sequence 46512, A	208	7	0.9	391	4	US-10-437-963-189621	Sequence 189621
136	7	0.9	200	4	US-10-425-115-279847	Sequence 279847,	209	7	0.9	398	4	US-10-425-114-71531	Sequence 71531, A
137	7	0.9	208	6	US-11-097-143-32487	Sequence 32487, A	210	7	0.9	401	4	US-10-424-599-269452	Sequence 269452
138	7	0.9	213	4	US-10-029-386-34063	Sequence 34063, A	211	7	0.9	405	4	US-10-369-493-8649	Sequence 8649, Ap
139	7	0.9	213	4	US-10-425-115-185030	Sequence 185030,	212	7	0.9	405	4	US-10-369-493-20689	Sequence 20689, A
140	7	0.9	217	4	US-10-425-114-39820	Sequence 39820, A	213	7	0.9	405	4	US-10-425-115-192417	Sequence 192417
141	7	0.9	220	4	US-10-437-963-187087	Sequence 187087,	214	7	0.9	411	4	US-10-369-493-12939	Sequence 12939, A
142	7	0.9	221	4	US-10-369-493-8397	Sequence 8397, Ap	215	7	0.9	416	4	US-10-282-122A-70224	Sequence 70224, A
143	7	0.9	221	4	US-10-425-115-337161	Sequence 337161,	216	7	0.9	417	5	US-10-450-763-33693	Sequence 33693, A
144	7	0.9	226	6	US-11-097-143-30105	Sequence 30105, A	217	7	0.9	423	5	US-10-450-763-58445	Sequence 58445, A
145	7	0.9	228	4	US-10-369-493-20929	Sequence 20929, A	218	7	0.9	425	4	US-10-117-018-8	Sequence 8, Appli
146	7	0.9	228	4	US-10-424-599-171239	Sequence 171239,	219	7	0.9	425	5	US-10-946-424-8	Sequence 8, Appli
147	7	0.9	234	3	US-09-882-227-24	Sequence 24, Appl	220	7	0.9	426	4	US-10-369-493-4635	Sequence 4635, Ap
148	7	0.9	234	4	US-10-335-977-8510	Sequence 8510, Ap	221	7	0.9	426	4	US-10-425-115-368617	Sequence 368617
149	7	0.9	234	4	US-10-425-115-185029	Sequence 185029,	222	7	0.9	426	5	US-10-732-923-10735	Sequence 10735, A
150	7	0.9	243	5	US-10-450-763-54612	Sequence 54612, A	223	7	0.9	429	4	US-10-282-122A-51466	Sequence 51466, A
151	7	0.9	245	4	US-10-425-115-351748	Sequence 351748,	224	7	0.9	432	4	US-10-437-963-182668	Sequence 182668
152	7	0.9	250	6	US-11-097-143-5376	Sequence 5376, Ap	225	7	0.9	433	4	US-10-282-122A-49892	Sequence 49892, A
153	7	0.9	254	4	US-10-395-607-127	Sequence 127, App	226	7	0.9	434	3	US-10-369-493-7393	Sequence 7393, Ap
154	7	0.9	254	4	US-10-799-870-127	Sequence 127, App	227	7	0.9	442	3	US-09-866-050A-641	Sequence 641, App
155	7	0.9	255	5	US-10-472-928-4076	Sequence 4076, Ap	228	7	0.9	444	4	US-10-369-493-6911	Sequence 6911, Ap
156	7	0.9	260	4	US-10-425-115-249662	Sequence 249662,	229	7	0.9	444	5	US-10-650-467-42	Sequence 42, Appl
157	7	0.9	262	4	US-10-424-599-232524	Sequence 232524,	230	7	0.9	444	5	US-10-450-763-38749	Sequence 38749, A
158	7	0.9	263	4	US-10-424-599-189044	Sequence 189044,	231	7	0.9	448	4	US-10-369-493-4105	Sequence 4105, Ap
159	7	0.9	272	4	US-10-437-963-201475	Sequence 201475,	232	7	0.9	456	4	US-10-369-493-20284	Sequence 20284, A
160	7	0.9	273	4	US-10-437-963-127798	Sequence 127798,	233	7	0.9	458	3	US-09-972-268-21	Sequence 21, Appl
161	7	0.9	274	4	US-10-437-963-116008	Sequence 116008,	234	7	0.9	458	4	US-10-299-636-99	Sequence 99, Appl
162	7	0.9	280	4	US-10-282-122A-74821	Sequence 74821, A	235	7	0.9	459	4	US-10-282-122A-70133	Sequence 70133, A
163	7	0.9	282	4	US-10-094-749-2096	Sequence 2096, Ap	236	7	0.9	464	3	US-09-912-020-281	Sequence 281, App
164	7	0.9	285	4	US-10-282-122A-72956	Sequence 72956, A	237	7	0.9	464	4	US-10-287-274-441	Sequence 441, App
165	7	0.9	288	4	US-10-369-493-22433	Sequence 22433, A	238	7	0.9	464	5	US-10-282-122A-42613	Sequence 42613, A
166	7	0.9	290	4	US-10-276-774-1357	Sequence 1357, Ap	239	7	0.9	464	5	US-10-771-241-281	Sequence 281, App
167	7	0.9	292	4	US-10-282-122A-57001	Sequence 57001, A	240	7	0.9	465	5	US-10-904-588-18	Sequence 18, Appl
168	7	0.9	293	4	US-10-369-493-13324	Sequence 13324, A	241	7	0.9	469	4	US-10-369-493-13381	Sequence 13381, A
169	7	0.9	301	4	US-10-156-761-13367	Sequence 13367, A	242	7	0.9	472	3	US-09-870-162A-3	Sequence 3, Appli
170	7	0.9	305	4	US-10-369-493-640	Sequence 640, App	243	7	0.9	478	5	US-10-469-204-141	Sequence 141, App
171	7	0.9	307	4	US-10-424-599-224191	Sequence 224191,	244	7	0.9	478	6	US-11-097-143-25683	Sequence 25683, A
172	7	0.9	308	4	US-10-156-761-14268	Sequence 14268, A	245	7	0.9	488	4	US-10-437-963-180174	Sequence 180174
173	7	0.9	308	5	US-10-732-923-10057	Sequence 10057, A	246	7	0.9	490	4	US-10-074-152-26	Sequence 26, Appl

247	7	0.9	497	3	US-09-815-242-13344	Sequence 13344, A	320	7	0.9	717	4	US-10-267-502-250	Sequence 250, App
248	7	0.9	497	4	US-10-282-122A-73912	Sequence 73912, A	321	7	0.9	717	6	US-11-097-143-11619	Sequence 11619, A
249	7	0.9	497	5	US-10-472-928-1718	Sequence 1718, Ap	322	7	0.9	732	4	US-10-184-644-577	Sequence 577, App
250	7	0.9	504	5	US-10-617-320-3732	Sequence 3732, A	323	7	0.9	732	4	US-10-184-634-577	Sequence 577, App
251	7	0.9	510	5	US-10-732-320-3732	Sequence 13923, A	324	7	0.9	711	4	US-10-282-122A-70070	Sequence 70070, A
252	7	0.9	514	4	US-10-161-572-60	Sequence 60, Appl	325	7	0.9	755	4	US-10-437-963-171603	Sequence 171603, A
253	7	0.9	517	3	US-09-975-268-20	Sequence 20, Appl	326	7	0.9	761	4	US-10-416-330-35	Sequence 35, Appl
254	7	0.9	518	3	US-09-919-172-20	Sequence 20, Appl	327	7	0.9	786	5	US-10-874-049-3	Sequence 3, Appl
255	7	0.9	518	4	US-10-369-493-18702	Sequence 18702, A	328	7	0.9	789	5	US-10-874-049-5	Sequence 5, Appl
256	7	0.9	518	5	US-10-752-986-20	Sequence 20, Appl	329	7	0.9	792	4	US-10-087-192-1977	Sequence 1977, Ap
257	7	0.9	521	4	US-10-282-122A-63634	Sequence 63634, A	330	7	0.9	792	5	US-10-450-763-46062	Sequence 46062, A
258	7	0.9	522	4	US-10-282-122A-50014	Sequence 50014, A	331	7	0.9	797	4	US-10-369-493-12480	Sequence 12480, A
259	7	0.9	527	4	US-10-282-122A-47475	Sequence 47475, A	332	7	0.9	818	3	US-09-738-626-6491	Sequence 6491, Ap
260	7	0.9	528	6	US-11-097-143-41799	Sequence 41799, A	333	7	0.9	823	4	US-10-437-963-104983	Sequence 104983, A
261	7	0.9	529	3	US-09-954-314-22	Sequence 22, Appl	334	7	0.9	823	6	US-11-097-143-41244	Sequence 1021, Ap
262	7	0.9	529	4	US-10-230-562-22	Sequence 22, Appl	335	7	0.9	850	4	US-10-238-075-1021	Sequence 12144, A
263	7	0.9	529	5	US-10-230-026-16	Sequence 16, Appl	336	7	0.9	874	4	US-10-282-122A-61488	Sequence 61488, A
264	7	0.9	529	5	US-10-739-930-9550	Sequence 9550, Ap	337	7	0.9	897	6	US-10-087-192-1977	Sequence 13575, A
265	7	0.9	529	5	US-10-486-307-16	Sequence 16, Appl	338	7	0.9	902	4	US-10-184-644-303	Sequence 303, App
266	7	0.9	539	4	US-10-424-599-227399	Sequence 227399, A	339	7	0.9	902	4	US-10-184-634-303	Sequence 93, Appl
267	7	0.9	545	5	US-10-287-436A-271	Sequence 271, App	340	7	0.9	902	4	US-10-063-685-93	Sequence 35, Appl
268	7	0.9	546	5	US-10-287-436A-212	Sequence 212, App	341	7	0.9	914	5	US-10-484-703-35	Sequence 1980, Ap
269	7	0.9	562	6	US-11-097-143-21426	Sequence 21426, A	342	7	0.9	933	4	US-10-087-192-1980	Sequence 3, Appl
270	7	0.9	564	5	US-10-739-930-9713	Sequence 9713, Ap	343	7	0.9	953	3	US-10-148-884-5	Sequence 5, Appl
271	7	0.9	564	5	US-10-481-113-28	Sequence 28, Appl	344	7	0.9	953	4	US-10-484-703-33	Sequence 337013, A
272	7	0.9	568	4	US-10-032-585-7920	Sequence 7920, Ap	345	7	0.9	956	5	US-10-080-608A-22	Sequence 22, Appl
273	7	0.9	572	4	US-10-437-963-173191	Sequence 173191, A	346	7	0.9	959	4	US-10-370-685-109	Sequence 109, App
274	7	0.9	572	5	US-10-481-113-104	Sequence 104, App	347	7	0.9	963	4	US-10-370-685-111	Sequence 111, App
275	7	0.9	572	5	US-10-481-032A-66	Sequence 66, Appl	348	7	0.9	963	4	US-11-009-554-10	Sequence 9, Appl
276	7	0.9	573	6	US-11-097-143-8811	Sequence 8811, Ap	349	7	0.9	967	6	US-10-478-245-9	Sequence 4153, Ap
277	7	0.9	578	4	US-10-425-115-249810	Sequence 249810, A	350	7	0.9	969	4	US-10-108-260A-4153	Sequence 194052, A
278	7	0.9	579	5	US-10-450-763-54609	Sequence 54609, A	351	7	0.9	978	4	US-10-425-115-194052	Sequence 4363, Ap
279	7	0.9	580	4	US-10-647-057-4	Sequence 4, Appl	352	7	0.9	992	4	US-09-738-626-4363	Sequence 69491, A
280	7	0.9	581	4	US-10-767-701-46924	Sequence 46924, A	353	7	0.9	1016	3	US-10-282-122A-69491	Sequence 1661, Ap
281	7	0.9	584	4	US-10-282-122A-47689	Sequence 47689, A	354	7	0.9	1019	4	US-10-408-765A-1661	Sequence 169433, A
282	7	0.9	587	3	US-09-893-519A-42	Sequence 42, Appl	355	7	0.9	1031	4	US-10-437-963-169433	Sequence 108, App
283	7	0.9	589	4	US-10-205-194-144	Sequence 144, App	356	7	0.9	1054	6	US-10-001-885-108	Sequence 108, App
284	7	0.9	589	4	US-10-437-963-127286	Sequence 127286, A	357	7	0.9	1054	6	US-11-057-447-108	Sequence 11583, A
285	7	0.9	590	5	US-10-831-070-10	Sequence 10, Appl	358	7	0.9	1078	6	US-11-097-143-11583	Sequence 152821, A
286	7	0.9	604	3	US-09-862-027-17	Sequence 17, Appl	359	7	0.9	1120	4	US-10-437-963-152821	Sequence 36, Appl
287	7	0.9	619	4	US-10-989-228-17	Sequence 17, Appl	360	7	0.9	1121	2	US-08-915-048A-2	Sequence 11, Appl
288	7	0.9	619	4	US-10-369-493-5855	Sequence 5855, Ap	361	7	0.9	1136	5	US-10-484-703-36	Sequence 5, Appl
289	7	0.9	620	3	US-09-893-519A-59	Sequence 59, Appl	362	7	0.9	1161	4	US-10-467-535-11	Sequence 353, App
290	7	0.9	620	4	US-10-369-493-1442	Sequence 22, Appl	363	7	0.9	1174	4	US-10-184-644-353	Sequence 353, App
291	7	0.9	622	4	US-10-197-666A-22	Sequence 22, Appl	364	7	0.9	1174	5	US-10-184-634-353	Sequence 34, Appl
292	7	0.9	622	4	US-10-024-298A-63	Sequence 63, Appl	365	7	0.9	1178	4	US-10-484-703-34	Sequence 1202, Ap
293	7	0.9	622	4	US-10-042-211A-63	Sequence 63, Appl	366	7	0.9	1248	4	US-10-389-566-1202	Sequence 188299, A
294	7	0.9	622	4	US-10-617-217A-63	Sequence 63, Appl	367	7	0.9	1264	4	US-10-123-155-1	Sequence 1, Appl
295	7	0.9	622	4	US-10-024-298A-63	Sequence 63, Appl	368	7	0.9	1264	4	US-10-146-731-1	Sequence 1, Appl
296	7	0.9	625	4	US-10-369-493-22882	Sequence 22882, A	369	7	0.9	1264	4	US-10-141-761-1	Sequence 1, Appl
297	7	0.9	627	5	US-10-450-763-48621	Sequence 48621, A	370	7	0.9	1264	4	US-10-142-885-1	Sequence 1, Appl
298	7	0.9	628	4	US-10-156-761-10990	Sequence 10990, A	371	7	0.9	1264	4	US-10-158-790-1	Sequence 1, Appl
299	7	0.9	628	5	US-10-450-763-54036	Sequence 54036, A	372	7	0.9	1264	4	US-10-137-871-1	Sequence 1, Appl
300	7	0.9	632	4	US-10-024-298A-65	Sequence 65, Appl	373	7	0.9	1264	4	US-10-140-923-1	Sequence 1, Appl
301	7	0.9	632	4	US-10-042-211A-65	Sequence 65, Appl	374	7	0.9	1264	4	US-10-141-759-1	Sequence 1, Appl
302	7	0.9	632	4	US-10-617-217A-65	Sequence 65, Appl	375	7	0.9	1264	4	US-10-140-805-1	Sequence 1, Appl
303	7	0.9	632	4	US-10-024-298A-65	Sequence 65, Appl	376	7	0.9	1264	4	US-10-140-864-1	Sequence 1, Appl
304	7	0.9	640	4	US-10-425-115-317987	Sequence 317987, A	377	7	0.9	1264	4	US-11-097-143-10734	Sequence 10734, A
305	7	0.9	649	6	US-11-097-143-10503	Sequence 10503, A	378	7	0.9	1264	6	US-10-302-279-60	Sequence 599, App
306	7	0.9	663	4	US-10-282-122A-52415	Sequence 52415, A	379	7	0.9	1297	4	US-10-184-644-599	Sequence 599, App
307	7	0.9	666	3	US-09-746-660A-46	Sequence 46, Appl	380	7	0.9	1297	4	US-10-184-634-599	Sequence 435, App
308	7	0.9	667	4	US-10-767-701-46248	Sequence 46248, A	381	7	0.9	1297	4	US-10-123-155-435	Sequence 435, App
309	7	0.9	667	5	US-10-450-763-47260	Sequence 47260, A	382	7	0.9	1297	4	US-10-146-731-435	Sequence 435, App
310	7	0.9	673	4	US-10-433-794-2	Sequence 2, Appl	383	7	0.9	1297	4	US-10-140-472-435	Sequence 435, App
311	7	0.9	676	5	US-10-617-362-4098	Sequence 4098, Ap	384	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
312	7	0.9	684	4	US-10-437-963-111247	Sequence 111247, A	385	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
313	7	0.9	686	4	US-10-282-122A-67777	Sequence 67777, A	386	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
314	7	0.9	692	4	US-10-369-493-8800	Sequence 8800, Ap	387	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
315	7	0.9	695	3	US-09-305-924-13	Sequence 13, Appl	388	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
316	7	0.9	699	4	US-10-156-761-12338	Sequence 12338, A	389	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
317	7	0.9	705	4	US-10-425-114-46512	Sequence 46512, A	390	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
318	7	0.9	711	4	US-10-425-114-54901	Sequence 54901, A	391	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App
319	7	0.9	711	4	US-10-425-115-317988	Sequence 317988, A	392	7	0.9	1297	4	US-10-141-761-435	Sequence 435, App

393	7	0.9	1297	4	US-10-142-885-435	Sequence 435, App	466	7	0.9	1484	4	US-10-141-761-447	Sequence 447, App
394	7	0.9	1297	4	US-10-158-790-435	Sequence 435, App	467	7	0.9	1484	4	US-10-142-885-447	Sequence 447, App
395	7	0.9	1297	4	US-10-137-871-435	Sequence 435, App	468	7	0.9	1484	4	US-10-158-790-447	Sequence 447, App
396	7	0.9	1297	4	US-10-140-923-435	Sequence 435, App	469	7	0.9	1484	4	US-10-137-871-447	Sequence 447, App
397	7	0.9	1297	4	US-10-141-756-435	Sequence 435, App	470	7	0.9	1484	4	US-10-140-923-447	Sequence 447, App
398	7	0.9	1297	4	US-10-141-759-435	Sequence 435, App	471	7	0.9	1484	4	US-10-141-756-447	Sequence 447, App
399	7	0.9	1297	4	US-10-140-805-435	Sequence 435, App	472	7	0.9	1484	4	US-10-141-759-447	Sequence 447, App
400	7	0.9	1297	4	US-10-140-864-435	Sequence 435, App	473	7	0.9	1484	4	US-10-140-805-447	Sequence 447, App
401	7	0.9	1320	4	US-10-161-051-167	Sequence 167, App	474	7	0.9	1484	4	US-10-140-864-447	Sequence 447, App
402	7	0.9	1334	4	US-10-184-644-339	Sequence 339, App	475	7	0.9	1515	4	US-10-184-634-399	Sequence 399, App
403	7	0.9	1334	4	US-10-184-634-339	Sequence 339, App	476	7	0.9	1515	4	US-10-184-634-339	Sequence 399, App
404	7	0.9	1336	4	US-10-224-999A-3482	Sequence 3482, Ap	477	7	0.9	1515	4	US-10-063-685-157	Sequence 157, App
405	7	0.9	1356	4	US-10-437-963-110486	Sequence 110486,	478	7	0.9	1536	4	US-10-184-644-461	Sequence 461, App
406	7	0.9	1376	4	US-10-123-155-161	Sequence 161, App	479	7	0.9	1536	4	US-10-184-634-461	Sequence 461, App
407	7	0.9	1376	4	US-10-146-731-161	Sequence 161, App	480	7	0.9	1576	4	US-10-335-977-5266	Sequence 5266, Ap
408	7	0.9	1376	4	US-10-140-472-161	Sequence 161, App	481	7	0.9	1584	5	US-10-732-923-12885	Sequence 12885, A
409	7	0.9	1376	4	US-10-141-761-161	Sequence 161, App	482	7	0.9	1624	4	US-10-123-155-181	Sequence 181, App
410	7	0.9	1376	4	US-10-142-885-161	Sequence 161, App	483	7	0.9	1624	4	US-10-146-731-181	Sequence 181, App
411	7	0.9	1376	4	US-10-158-790-161	Sequence 161, App	484	7	0.9	1624	4	US-10-140-472-181	Sequence 181, App
412	7	0.9	1376	4	US-10-137-871-161	Sequence 161, App	485	7	0.9	1624	4	US-10-141-761-181	Sequence 181, App
413	7	0.9	1376	4	US-10-140-923-161	Sequence 161, App	486	7	0.9	1624	4	US-10-142-885-181	Sequence 181, App
414	7	0.9	1376	4	US-10-141-756-161	Sequence 161, App	487	7	0.9	1624	4	US-10-158-790-181	Sequence 181, App
415	7	0.9	1376	4	US-10-141-759-161	Sequence 161, App	488	7	0.9	1624	4	US-10-137-871-181	Sequence 181, App
416	7	0.9	1376	4	US-10-140-805-161	Sequence 161, App	489	7	0.9	1624	4	US-10-140-923-181	Sequence 181, App
417	7	0.9	1376	4	US-10-140-864-161	Sequence 161, App	490	7	0.9	1624	4	US-10-141-756-181	Sequence 181, App
418	7	0.9	1390	4	US-10-137-418A-2	Sequence 2, Appli	491	7	0.9	1624	4	US-10-141-753-181	Sequence 181, App
419	7	0.9	1419	4	US-10-123-155-517	Sequence 517, App	492	7	0.9	1624	4	US-10-140-805-181	Sequence 181, App
420	7	0.9	1419	4	US-10-146-731-517	Sequence 517, App	493	7	0.9	1624	4	US-10-140-864-181	Sequence 181, App
421	7	0.9	1419	4	US-10-140-472-517	Sequence 517, App	494	7	0.9	1628	5	US-10-450-763-32554	Sequence 32554, A
422	7	0.9	1419	4	US-10-141-761-517	Sequence 517, App	495	7	0.9	1665	4	US-10-184-644-285	Sequence 285, App
423	7	0.9	1419	4	US-10-142-885-517	Sequence 517, App	496	7	0.9	1665	4	US-10-184-634-285	Sequence 285, App
424	7	0.9	1419	4	US-10-158-790-517	Sequence 517, App	497	7	0.9	1665	4	US-10-063-685-85	Sequence 85, Appl
425	7	0.9	1419	4	US-10-137-871-517	Sequence 517, App	498	7	0.9	1686	4	US-10-092-219-2	Sequence 2, Appli
426	7	0.9	1419	4	US-10-140-923-517	Sequence 517, App	499	7	0.9	1730	4	US-10-123-155-7	Sequence 7, Appli
427	7	0.9	1419	4	US-10-141-756-517	Sequence 517, App	500	7	0.9	1730	4	US-10-146-731-7	Sequence 7, Appli
428	7	0.9	1419	4	US-10-141-759-517	Sequence 517, App	501	7	0.9	1730	4	US-10-140-472-7	Sequence 7, Appli
429	7	0.9	1419	4	US-10-140-805-517	Sequence 517, App	502	7	0.9	1730	4	US-10-141-761-7	Sequence 7, Appli
430	7	0.9	1419	4	US-10-140-864-517	Sequence 517, App	503	7	0.9	1730	4	US-10-142-885-7	Sequence 7, Appli
431	7	0.9	1419	4	US-10-092-900A-82	Sequence 82, Appl	504	7	0.9	1730	4	US-10-158-790-7	Sequence 7, Appli
432	7	0.9	1423	4	US-10-092-900A-86	Sequence 86, Appl	505	7	0.9	1730	4	US-10-137-871-7	Sequence 7, Appli
433	7	0.9	1434	2	US-08-954-701A-10	Sequence 10, Appl	506	7	0.9	1730	4	US-10-140-923-7	Sequence 7, Appli
434	7	0.9	1434	3	US-09-754-032-10	Sequence 10, Appl	507	7	0.9	1730	4	US-10-141-756-7	Sequence 7, Appli
435	7	0.9	1434	4	US-10-421-446-10	Sequence 10, Appl	508	7	0.9	1730	4	US-10-141-759-7	Sequence 7, Appli
436	7	0.9	1439	4	US-10-220-481-73	Sequence 73, Appl	509	7	0.9	1730	4	US-10-140-805-7	Sequence 7, Appli
437	7	0.9	1447	2	US-08-954-701A-19	Sequence 19, Appl	510	7	0.9	1771	4	US-10-140-864-7	Sequence 7, Appli
438	7	0.9	1447	3	US-09-898-533-5	Sequence 5, Appli	511	7	0.9	1771	4	US-10-184-634-17	Sequence 17, Appl
439	7	0.9	1447	3	US-09-754-032-19	Sequence 19, Appl	512	7	0.9	1771	4	US-10-184-634-17	Sequence 17, Appl
440	7	0.9	1447	4	US-10-421-446-19	Sequence 19, Appl	513	7	0.9	1775	4	US-10-335-977-5267	Sequence 5267, Ap
441	7	0.9	1447	4	US-10-791-844-6	Sequence 6, Appli	514	7	0.9	1808	4	US-10-123-155-47	Sequence 47, Appl
442	7	0.9	1449	4	US-10-282-122A-65711	Sequence 65711, A	515	7	0.9	1808	4	US-10-146-731-47	Sequence 47, Appl
443	7	0.9	1454	4	US-10-742-345-2	Sequence 2, Appli	516	7	0.9	1808	4	US-10-140-472-47	Sequence 47, Appl
444	7	0.9	1455	5	US-10-484-703-32	Sequence 32, Appl	517	7	0.9	1808	4	US-10-141-761-47	Sequence 47, Appl
445	7	0.9	1457	4	US-10-220-481-71	Sequence 71, Appl	518	7	0.9	1808	4	US-10-142-885-47	Sequence 47, Appl
446	7	0.9	1457	4	US-10-742-345-4	Sequence 4, Appli	519	7	0.9	1808	4	US-10-158-790-47	Sequence 47, Appl
447	7	0.9	1457	5	US-10-915-7A0A-1047	Sequence 1047, Ap	520	7	0.9	1808	4	US-10-137-871-47	Sequence 47, Appl
448	7	0.9	1458	4	US-10-054-691-2	Sequence 2, Appli	521	7	0.9	1808	4	US-10-140-923-47	Sequence 47, Appl
449	7	0.9	1458	4	US-10-478-245-1	Sequence 1, Appli	522	7	0.9	1808	4	US-10-141-756-47	Sequence 47, Appl
450	7	0.9	1468	4	US-10-282-122A-65027	Sequence 65027, A	523	7	0.9	1808	4	US-10-141-759-47	Sequence 47, Appl
451	7	0.9	1471	4	US-10-123-155-281	Sequence 281, App	524	7	0.9	1808	4	US-10-140-805-47	Sequence 47, Appl
452	7	0.9	1471	4	US-10-146-731-281	Sequence 281, App	525	7	0.9	1808	4	US-10-140-864-47	Sequence 47, Appl
453	7	0.9	1471	4	US-10-140-472-281	Sequence 281, App	526	7	0.9	1849	4	US-10-184-644-133	Sequence 133, App
454	7	0.9	1471	4	US-10-141-761-281	Sequence 281, App	527	7	0.9	1849	4	US-10-184-634-133	Sequence 133, App
455	7	0.9	1471	4	US-10-142-885-281	Sequence 281, App	528	7	0.9	1849	4	US-10-063-685-21	Sequence 21, Appl
456	7	0.9	1471	4	US-10-158-790-281	Sequence 281, App	529	7	0.9	1883	4	US-10-123-155-501	Sequence 501, App
457	7	0.9	1471	4	US-10-137-871-281	Sequence 281, App	530	7	0.9	1883	4	US-10-146-731-501	Sequence 501, App
458	7	0.9	1471	4	US-10-140-923-281	Sequence 281, App	531	7	0.9	1883	4	US-10-140-472-501	Sequence 501, App
459	7	0.9	1471	4	US-10-141-756-281	Sequence 281, App	532	7	0.9	1883	4	US-10-141-761-501	Sequence 501, App
460	7	0.9	1471	4	US-10-141-759-281	Sequence 281, App	533	7	0.9	1883	4	US-10-142-885-501	Sequence 501, App
461	7	0.9	1471	4	US-10-140-805-281	Sequence 281, App	534	7	0.9	1883	4	US-10-158-790-501	Sequence 501, App
462	7	0.9	1471	4	US-10-140-864-281	Sequence 281, App	535	7	0.9	1883	4	US-10-137-871-501	Sequence 501, App
463	7	0.9	1484	4	US-10-123-155-447	Sequence 447, App	536	7	0.9	1883	4	US-10-140-923-501	Sequence 501, App
464	7	0.9	1484	4	US-10-146-731-447	Sequence 447, App	537	7	0.9	1883	4	US-10-141-756-501	Sequence 501, App
465	7	0.9	1484	4	US-10-140-472-447	Sequence 447, App	538	7	0.9	1883	4	US-10-141-759-501	Sequence 501, App

539	7	0.9	1883	4	US-10-140-805-501	Sequence 501, App	612	7	0.9	2457	4	US-10-184-644-569	Sequence 569, App
540	7	0.9	1883	4	US-10-140-864-501	Sequence 501, App	613	7	0.9	2457	4	US-10-184-634-569	Sequence 569, App
541	7	0.9	1912	4	US-10-188-186-48	Sequence 48, Appli	614	7	0.9	2478	4	US-10-184-644-107	Sequence 107, App
542	7	0.9	1943	4	US-10-282-122A-58750	Sequence 58750, A	615	7	0.9	2478	4	US-10-184-634-107	Sequence 107, App
543	7	0.9	1974	3	US-09-895-913A-12	Sequence 12, Appl	616	7	0.9	2497	5	US-10-481-582-4	Sequence 4, Appli
544	7	0.9	1975	4	US-10-123-155-105	Sequence 105, App	617	7	0.9	2558	4	US-10-184-644-103	Sequence 103, App
545	7	0.9	1975	4	US-10-146-731-105	Sequence 105, App	618	7	0.9	2558	4	US-10-184-634-103	Sequence 103, App
546	7	0.9	1975	4	US-10-140-472-105	Sequence 105, App	619	7	0.9	2594	4	US-10-123-155-245	Sequence 245, App
547	7	0.9	1975	4	US-10-140-472-105	Sequence 105, App	620	7	0.9	2594	4	US-10-146-731-245	Sequence 245, App
548	7	0.9	1975	4	US-10-141-761-105	Sequence 105, App	621	7	0.9	2594	4	US-10-140-472-245	Sequence 245, App
549	7	0.9	1975	4	US-10-142-885-105	Sequence 105, App	622	7	0.9	2594	4	US-10-141-761-245	Sequence 245, App
550	7	0.9	1975	4	US-10-158-790-105	Sequence 105, App	623	7	0.9	2594	4	US-10-142-885-245	Sequence 245, App
551	7	0.9	1975	4	US-10-137-871-105	Sequence 105, App	624	7	0.9	2594	4	US-10-158-790-245	Sequence 245, App
552	7	0.9	1975	4	US-10-140-923-105	Sequence 105, App	625	7	0.9	2594	4	US-10-137-871-245	Sequence 245, App
553	7	0.9	1975	4	US-10-141-756-105	Sequence 105, App	626	7	0.9	2594	4	US-10-146-731-245	Sequence 245, App
554	7	0.9	1975	4	US-10-141-759-105	Sequence 105, App	627	7	0.9	2594	4	US-10-141-756-245	Sequence 245, App
555	7	0.9	1975	4	US-10-140-805-105	Sequence 105, App	628	7	0.9	2594	4	US-10-141-759-245	Sequence 245, App
556	7	0.9	1975	4	US-10-140-864-105	Sequence 105, App	629	7	0.9	2594	4	US-10-140-805-245	Sequence 245, App
557	7	0.9	1984	5	US-10-450-763-31697	Sequence 31697, A	630	7	0.9	2594	4	US-10-140-864-245	Sequence 245, App
558	7	0.9	2037	4	US-10-184-644-591	Sequence 591, App	631	7	0.9	2598	4	US-10-063-685-151	Sequence 151, App
559	7	0.9	2037	4	US-10-184-634-591	Sequence 591, App	632	7	0.9	2609	4	US-10-184-644-407	Sequence 407, App
560	7	0.9	2055	5	US-10-481-582-3	Sequence 3, Appli	633	7	0.9	2609	4	US-10-184-634-407	Sequence 407, App
561	7	0.9	2103	4	US-10-184-644-319	Sequence 319, App	634	7	0.9	2615	4	US-10-184-644-523	Sequence 523, App
562	7	0.9	2103	4	US-10-184-634-319	Sequence 319, App	635	7	0.9	2615	4	US-10-184-634-523	Sequence 523, App
563	7	0.9	2134	4	US-10-063-685-105	Sequence 105, App	636	7	0.9	2732	4	US-10-238-075-1119	Sequence 1119, App
564	7	0.9	2134	4	US-10-123-155-179	Sequence 179, App	637	7	0.9	2819	4	US-10-184-644-109	Sequence 109, App
565	7	0.9	2134	4	US-10-146-731-179	Sequence 179, App	638	7	0.9	2819	4	US-10-184-634-109	Sequence 109, App
566	7	0.9	2134	4	US-10-140-472-179	Sequence 179, App	639	7	0.9	2834	4	US-10-085-959-252	Sequence 252, App
567	7	0.9	2134	4	US-10-141-761-179	Sequence 179, App	640	7	0.9	2916	4	US-10-123-155-69	Sequence 69, Appl
568	7	0.9	2134	4	US-10-142-885-179	Sequence 179, App	641	7	0.9	2916	4	US-10-146-731-69	Sequence 69, Appl
569	7	0.9	2134	4	US-10-158-790-179	Sequence 179, App	642	7	0.9	2916	4	US-10-140-472-69	Sequence 69, Appl
570	7	0.9	2134	4	US-10-137-871-179	Sequence 179, App	643	7	0.9	2916	4	US-10-140-472-69	Sequence 69, Appl
571	7	0.9	2134	4	US-10-140-923-179	Sequence 179, App	644	7	0.9	2916	4	US-10-141-761-69	Sequence 69, Appl
572	7	0.9	2134	4	US-10-141-756-179	Sequence 179, App	645	7	0.9	2916	4	US-10-142-885-69	Sequence 69, Appl
573	7	0.9	2134	4	US-10-140-805-179	Sequence 179, App	646	7	0.9	2916	4	US-10-158-790-69	Sequence 69, Appl
574	7	0.9	2134	4	US-10-140-864-179	Sequence 179, App	647	7	0.9	2916	4	US-10-137-871-69	Sequence 69, Appl
575	7	0.9	2237	4	US-10-123-155-45	Sequence 45, Appl	648	7	0.9	2916	4	US-10-140-923-69	Sequence 69, Appl
576	7	0.9	2237	4	US-10-146-731-45	Sequence 45, Appl	649	7	0.9	2916	4	US-10-141-756-69	Sequence 69, Appl
577	7	0.9	2237	4	US-10-140-472-45	Sequence 45, Appl	650	7	0.9	2916	4	US-10-140-805-69	Sequence 69, Appl
578	7	0.9	2237	4	US-10-141-761-45	Sequence 45, Appl	651	7	0.9	2916	4	US-10-141-759-69	Sequence 69, Appl
579	7	0.9	2237	4	US-10-142-885-45	Sequence 45, Appl	652	7	0.9	2916	4	US-10-140-805-69	Sequence 69, Appl
580	7	0.9	2237	4	US-10-158-790-45	Sequence 45, Appl	653	7	0.9	2956	4	US-10-140-864-69	Sequence 69, Appl
581	7	0.9	2237	4	US-10-137-871-45	Sequence 45, Appl	654	7	0.9	2956	4	US-10-184-644-73	Sequence 73, Appl
582	7	0.9	2237	4	US-10-140-923-45	Sequence 45, Appl	655	7	0.9	3033	4	US-10-184-634-1	Sequence 1, Appli
583	7	0.9	2237	4	US-10-141-756-45	Sequence 45, Appl	656	7	0.9	3033	4	US-10-184-634-1	Sequence 1, Appli
584	7	0.9	2237	4	US-10-141-759-45	Sequence 45, Appl	657	7	0.9	3038	4	US-10-184-644-261	Sequence 261, App
585	7	0.9	2237	4	US-10-140-805-45	Sequence 45, Appl	658	7	0.9	3089	4	US-10-184-634-61	Sequence 61, Appl
586	7	0.9	2274	4	US-10-140-864-45	Sequence 45, Appl	659	7	0.9	3089	4	US-10-184-634-61	Sequence 61, Appl
587	7	0.9	2274	4	US-10-267-502-373	Sequence 373, App	660	7	0.9	3122	4	US-10-200-562-201	Sequence 201, App
588	7	0.9	2274	5	US-10-805-684-140	Sequence 140, App	661	7	0.9	3122	4	US-10-237-551-201	Sequence 201, App
589	7	0.9	2275	4	US-10-184-644-401	Sequence 401, App	662	7	0.9	3122	4	US-10-237-551-250	Sequence 250, App
590	7	0.9	2275	4	US-10-184-634-401	Sequence 401, App	663	7	0.9	3122	5	US-10-945-050-201	Sequence 201, App
591	7	0.9	2303	4	US-10-267-502-371	Sequence 371, App	664	7	0.9	3122	5	US-10-945-050-250	Sequence 250, App
592	7	0.9	2303	5	US-10-852-335A-109	Sequence 109, App	665	7	0.9	3150	4	US-10-184-644-81	Sequence 81, Appl
593	7	0.9	2338	4	US-10-029-386-31982	Sequence 31982, A	666	7	0.9	3150	4	US-10-184-634-81	Sequence 81, Appl
594	7	0.9	2387	4	US-10-123-155-527	Sequence 527, App	667	7	0.9	3192	4	US-10-123-155-75	Sequence 75, Appl
595	7	0.9	2387	4	US-10-146-731-527	Sequence 527, App	668	7	0.9	3192	4	US-10-146-731-75	Sequence 75, Appl
596	7	0.9	2387	4	US-10-140-472-527	Sequence 527, App	669	7	0.9	3192	4	US-10-140-472-75	Sequence 75, Appl
597	7	0.9	2387	4	US-10-141-761-527	Sequence 527, App	670	7	0.9	3192	4	US-10-141-761-75	Sequence 75, Appl
598	7	0.9	2387	4	US-10-142-885-527	Sequence 527, App	671	7	0.9	3192	4	US-10-142-885-75	Sequence 75, Appl
599	7	0.9	2387	4	US-10-158-790-527	Sequence 527, App	672	7	0.9	3192	4	US-10-158-790-75	Sequence 75, Appl
600	7	0.9	2387	4	US-10-137-871-527	Sequence 527, App	673	7	0.9	3192	4	US-10-137-871-75	Sequence 75, Appl
601	7	0.9	2387	4	US-10-140-923-527	Sequence 527, App	674	7	0.9	3192	4	US-10-140-923-75	Sequence 75, Appl
602	7	0.9	2387	4	US-10-141-756-527	Sequence 527, App	675	7	0.9	3192	4	US-10-141-759-75	Sequence 75, Appl
603	7	0.9	2387	4	US-10-141-759-527	Sequence 527, App	676	7	0.9	3192	4	US-10-140-805-75	Sequence 75, Appl
604	7	0.9	2387	4	US-10-140-805-527	Sequence 527, App	677	7	0.9	3192	4	US-10-140-805-75	Sequence 75, Appl
605	7	0.9	2387	4	US-10-140-864-527	Sequence 527, App	678	7	0.9	3192	4	US-10-140-864-75	Sequence 75, Appl
606	7	0.9	2397	4	US-10-184-644-29	Sequence 29, Appl	679	7	0.9	3194	4	US-10-282-122A-59046	Sequence 59046, A
607	7	0.9	2397	4	US-10-184-644-323	Sequence 323, App	680	7	0.9	3233	4	US-10-123-155-81	Sequence 81, Appl
608	7	0.9	2397	4	US-10-184-634-29	Sequence 29, Appl	681	7	0.9	3233	4	US-10-146-731-81	Sequence 81, Appl
609	7	0.9	2397	4	US-10-184-634-323	Sequence 323, App	682	7	0.9	3233	4	US-10-140-472-81	Sequence 81, Appl
610	7	0.9	2397	4	US-10-063-685-107	Sequence 107, App	683	7	0.9	3233	4	US-10-141-761-81	Sequence 81, Appl
611	7	0.9	2431	3	US-09-901-106-2	Sequence 2, Appli	684	7	0.9	3233	4	US-10-142-885-81	Sequence 81, Appl

685	7	0.9	3233	4	US-10-158-790-81	Sequence 81, Appl	758	6	0.8	9	3	US-09-935-384-219	Sequence 219, App
686	7	0.9	3233	4	US-10-137-871-81	Sequence 81, Appl	759	6	0.8	9	3	US-09-935-384-447	Sequence 447, App
687	7	0.9	3233	4	US-10-140-923-81	Sequence 81, Appl	760	6	0.8	9	3	US-09-935-384-613	Sequence 613, App
688	7	0.9	3233	4	US-10-141-756-81	Sequence 81, Appl	761	6	0.8	10	3	US-09-572-404B-512	Sequence 512, App
689	7	0.9	3233	4	US-10-141-759-81	Sequence 81, Appl	762	6	0.8	10	3	US-09-935-384-158	Sequence 158, App
690	7	0.9	3233	4	US-10-140-805-81	Sequence 81, Appl	763	6	0.8	10	3	US-09-935-384-266	Sequence 266, App
691	7	0.9	3233	4	US-10-140-864-81	Sequence 81, Appl	764	6	0.8	10	3	US-09-935-384-268	Sequence 268, App
692	7	0.9	3240	4	US-10-184-644-415	Sequence 415, App	765	6	0.8	10	3	US-09-935-384-473	Sequence 473, App
693	7	0.9	3240	4	US-10-184-634-415	Sequence 415, App	766	6	0.8	10	3	US-09-935-384-573	Sequence 573, App
694	7	0.9	3323	4	US-10-123-155-167	Sequence 167, App	767	6	0.8	10	4	US-10-319-340-4	Sequence 4, Appli
695	7	0.9	3323	4	US-10-146-731-167	Sequence 167, App	768	6	0.8	10	4	US-10-319-340-5	Sequence 5, Appli
696	7	0.9	3323	4	US-10-140-472-167	Sequence 167, App	769	6	0.8	10	4	US-10-319-340-6	Sequence 6, Appli
697	7	0.9	3323	4	US-10-141-761-167	Sequence 167, App	770	6	0.8	10	4	US-10-319-340-19	Sequence 19, Appl
698	7	0.9	3323	4	US-10-142-885-167	Sequence 167, App	771	6	0.8	10	4	US-10-297-969-2	Sequence 2, Appli
699	7	0.9	3323	4	US-10-158-790-167	Sequence 167, App	772	6	0.8	11	5	US-10-862-195-2159	Sequence 2159, App
700	7	0.9	3323	4	US-10-137-871-167	Sequence 167, App	773	6	0.8	11	5	US-10-946-647-171	Sequence 171, App
701	7	0.9	3323	4	US-10-140-923-167	Sequence 167, App	774	6	0.8	11	5	US-10-946-647-399	Sequence 399, App
702	7	0.9	3323	4	US-10-141-756-167	Sequence 167, App	775	6	0.8	11	5	US-10-946-647-530	Sequence 530, App
703	7	0.9	3323	4	US-10-141-759-167	Sequence 167, App	776	6	0.8	11	5	US-10-946-647-700	Sequence 700, App
704	7	0.9	3323	4	US-10-140-805-167	Sequence 167, App	777	6	0.8	12	4	US-10-700-330-137	Sequence 137, App
705	7	0.9	3323	4	US-10-140-864-167	Sequence 167, App	778	6	0.8	13	4	US-10-411-869A-53	Sequence 53, Appl
706	7	0.9	3401	4	US-10-184-644-411	Sequence 411, App	779	6	0.8	14	4	US-10-312-691-6	Sequence 6, Appli
707	7	0.9	3401	4	US-10-184-634-411	Sequence 411, App	780	6	0.8	14	5	US-10-813-638-1304	Sequence 1304, Ap
708	7	0.9	3552	4	US-10-123-155-339	Sequence 339, App	781	6	0.8	15	3	US-09-880-748-2970	Sequence 2970, Ap
709	7	0.9	3552	4	US-10-146-731-339	Sequence 339, App	782	6	0.8	15	4	US-10-293-418-2970	Sequence 2970, Ap
710	7	0.9	3552	4	US-10-140-472-339	Sequence 339, App	783	6	0.8	15	4	US-10-412-964-68	Sequence 68, Appl
711	7	0.9	3552	4	US-10-141-761-339	Sequence 339, App	784	6	0.8	16	5	US-10-862-195-1036	Sequence 1036, Ap
712	7	0.9	3552	4	US-10-142-885-339	Sequence 339, App	785	6	0.8	18	4	US-10-187-496A-20	Sequence 20, Appl
713	7	0.9	3552	4	US-10-158-790-339	Sequence 339, App	786	6	0.8	18	5	US-10-946-647-402	Sequence 402, App
714	7	0.9	3552	4	US-10-137-871-339	Sequence 339, App	787	6	0.8	19	3	US-09-932-923-1	Sequence 1, Appli
715	7	0.9	3552	4	US-10-140-923-339	Sequence 339, App	788	6	0.8	19	4	US-10-297-969-6	Sequence 6, Appli
716	7	0.9	3552	4	US-10-141-756-339	Sequence 339, App	789	6	0.8	21	4	US-10-449-735-3	Sequence 3, Appli
717	7	0.9	3552	4	US-10-141-759-339	Sequence 339, App	790	6	0.8	23	4	US-10-097-065-356	Sequence 356, App
718	7	0.9	3552	4	US-10-140-805-339	Sequence 339, App	791	6	0.8	23	4	US-10-372-876-356	Sequence 356, App
719	7	0.9	3552	4	US-10-140-864-339	Sequence 339, App	792	6	0.8	24	3	US-09-843-221A-129	Sequence 129, App
720	7	0.9	3871	4	US-10-184-644-347	Sequence 347, App	793	6	0.8	24	3	US-09-843-221A-130	Sequence 130, App
721	7	0.9	3871	4	US-10-184-634-347	Sequence 347, App	794	6	0.8	24	3	US-09-999-608-129	Sequence 129, App
722	7	0.9	4040	4	US-10-123-155-425	Sequence 425, App	795	6	0.8	24	3	US-09-999-608-130	Sequence 130, App
723	7	0.9	4040	4	US-10-146-731-425	Sequence 425, App	796	6	0.8	24	4	US-10-425-115-338692	Sequence 338692,
724	7	0.9	4040	4	US-10-140-472-425	Sequence 425, App	797	6	0.8	24	4	US-10-839-037-129	Sequence 129, App
725	7	0.9	4040	4	US-10-141-761-425	Sequence 425, App	798	6	0.8	24	4	US-10-839-037-130	Sequence 130, App
726	7	0.9	4040	4	US-10-142-885-425	Sequence 425, App	799	6	0.8	25	3	US-09-911-888-35	Sequence 35, Appl
727	7	0.9	4040	4	US-10-158-790-425	Sequence 425, App	800	6	0.8	25	3	US-09-911-927-35	Sequence 35, Appl
728	7	0.9	4040	4	US-10-137-871-425	Sequence 425, App	801	6	0.8	26	4	US-10-242-355-472	Sequence 472, App
729	7	0.9	4040	4	US-10-140-923-425	Sequence 425, App	802	6	0.8	26	5	US-10-946-647-1362	Sequence 1362, Ap
730	7	0.9	4040	4	US-10-141-756-425	Sequence 425, App	803	6	0.8	28	3	US-09-843-221A-93	Sequence 93, Appl
731	7	0.9	4040	4	US-10-141-759-425	Sequence 425, App	804	6	0.8	28	3	US-09-843-221A-94	Sequence 94, Appl
732	7	0.9	4040	4	US-10-140-805-425	Sequence 425, App	805	6	0.8	28	3	US-09-999-608-93	Sequence 93, Appl
733	7	0.9	4040	4	US-10-140-864-425	Sequence 425, App	806	6	0.8	28	3	US-09-999-608-94	Sequence 94, Appl
734	7	0.9	4060	4	US-10-123-155-197	Sequence 197, App	807	6	0.8	28	4	US-10-261-208-4	Sequence 4, Appli
735	7	0.9	4060	4	US-10-146-731-197	Sequence 197, App	808	6	0.8	28	4	US-10-424-599-156146	Sequence 156146,
736	7	0.9	4060	4	US-10-140-472-197	Sequence 197, App	809	6	0.8	28	4	US-10-839-037-93	Sequence 93, Appl
737	7	0.9	4060	4	US-10-141-761-197	Sequence 197, App	810	6	0.8	28	4	US-10-839-037-94	Sequence 94, Appl
738	7	0.9	4060	4	US-10-142-885-197	Sequence 197, App	811	6	0.8	28	5	US-10-926-683-1203	Sequence 1203, Ap
739	7	0.9	4060	4	US-10-158-790-197	Sequence 197, App	812	6	0.8	28	5	US-10-915-740A-1051	Sequence 1051, Ap
740	7	0.9	4060	4	US-10-137-871-197	Sequence 197, App	813	6	0.8	30	3	US-09-843-221A-124	Sequence 124, App
741	7	0.9	4060	4	US-10-140-923-197	Sequence 197, App	814	6	0.8	30	3	US-09-843-221A-125	Sequence 125, App
742	7	0.9	4060	4	US-10-141-756-197	Sequence 197, App	815	6	0.8	30	3	US-09-843-221A-158	Sequence 158, App
743	7	0.9	4060	4	US-10-141-759-197	Sequence 197, App	816	6	0.8	30	3	US-09-999-608-124	Sequence 124, App
744	7	0.9	4060	4	US-10-140-805-197	Sequence 197, App	817	6	0.8	30	3	US-09-999-608-125	Sequence 125, App
745	7	0.9	4060	4	US-10-140-864-197	Sequence 197, App	818	6	0.8	30	3	US-09-999-608-158	Sequence 158, App
746	7	0.9	4106	3	US-09-980-217-23	Sequence 23, Appl	819	6	0.8	30	4	US-10-437-963-138633	Sequence 138633,
747	7	0.9	4106	5	US-10-732-923-20549	Sequence 20549, A	820	6	0.8	30	4	US-10-839-037-124	Sequence 124, App
748	7	0.9	4640	4	US-10-184-644-75	Sequence 75, Appl	821	6	0.8	30	4	US-10-839-037-125	Sequence 125, App
749	7	0.9	4640	4	US-10-184-634-75	Sequence 75, Appl	822	6	0.8	30	4	US-10-839-037-158	Sequence 158, App
750	7	0.9	4679	3	US-09-804-898-2	Sequence 2, Appli	823	6	0.8	31	4	US-10-097-079-50	Sequence 50, Appl
751	7	0.9	4999	3	US-09-976-059-14	Sequence 14, Appl	824	6	0.8	33	3	US-09-864-761-35842	Sequence 35842, A
752	7	0.9	8026	4	US-10-132-134-12	Sequence 12, Appl	825	6	0.8	33	4	US-10-000-256A-175	Sequence 175, App
753	7	0.9	18636	4	US-10-073-912-17	Sequence 17, Appl	826	6	0.8	33	4	US-10-029-386-33592	Sequence 33592, A
754	7	0.9	35346	5	US-10-874-049-2	Sequence 2, Appli	827	6	0.8	33	4	US-10-424-599-205494	Sequence 205494,
755	7	0.9	35823	5	US-10-874-049-1	Sequence 1, Appli	828	6	0.8	34	3	US-09-843-221A-88	Sequence 88, Appl
756	7	0.9	36946	5	US-10-840-512-155	Sequence 155, App	829	6	0.8	34	3	US-09-843-221A-89	Sequence 89, Appl
757	6	0.8	9	3	US-09-935-384-116	Sequence 116, App	830	6	0.8	34	3	US-09-843-221A-122	Sequence 122, App

831	6	0.8	34	3	US-09-935-384-755	Sequence 755, App	904	53	4	US-10-425-115-273363	Sequence 273363,
832	6	0.8	34	3	US-09-935-384-756	Sequence 756, App	905	54	4	US-10-424-599-192315	Sequence 192315,
833	6	0.8	34	3	US-09-999-608-88	Sequence 88, App	906	54	4	US-10-424-599-236359	Sequence 236359,
834	6	0.8	34	3	US-09-999-608-89	Sequence 89, App	907	54	4	US-10-425-115-211925	Sequence 211925,
835	6	0.8	34	3	US-09-999-608-122	Sequence 122, App	908	54	4	US-10-425-115-261837	Sequence 261837,
836	6	0.8	34	4	US-10-282-122A-70169	Sequence 70169, A	909	54	4	US-10-425-115-308996	Sequence 308996,
837	6	0.8	34	4	US-10-425-115-265306	Sequence 265306,	910	54	4	US-10-425-115-333948	Sequence 333948,
838	6	0.8	34	4	US-10-839-037-88	Sequence 88, App	911	54	5	US-10-808-187-1904	Sequence 1904, App
839	6	0.8	34	4	US-10-839-037-89	Sequence 89, App	912	54	5	US-10-807-807-1904	Sequence 1904, App
840	6	0.8	34	4	US-10-839-037-122	Sequence 122, App	913	55	3	US-09-864-761-47472	Sequence 47472, A
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844	6	0.8	36	4	US-10-437-963-195293	Sequence 195293,	917	56	3	US-09-939-980-332	Sequence 332, App
845	6	0.8	36	4	US-10-425-115-262724	Sequence 262724,	918	56	4	US-10-424-599-181170	Sequence 181170,
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848	6	0.8	39	4	US-10-029-386-30437	Sequence 30437, A	921	56	4	US-10-424-599-193599	Sequence 193599,
849	6	0.8	39	4	US-10-425-115-367446	Sequence 367446,	922	57	3	US-09-864-761-46468	Sequence 46468, A
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858	6	0.8	43	4	US-10-424-599-254844	Sequence 254844,	931	58	5	US-09-864-761-42686	Sequence 42686, A
859	6	0.8	43	4	US-10-767-701-61514	Sequence 61514, A	932	59	3	US-10-424-599-187445	Sequence 187445,
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861	6	0.8	44	3	US-09-925-299-1094	Sequence 1094, App	934	59	4	US-10-767-701-33262	Sequence 33262, A
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865	6	0.8	44	4	US-10-424-599-181073	Sequence 181073,	938	59	4	US-10-425-115-326057	Sequence 326057,
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868	6	0.8	45	4	US-10-424-599-200405	Sequence 200405,	941	60	3	US-09-935-384-773	Sequence 773, App
869	6	0.8	45	4	US-10-425-115-215060	Sequence 215060,	942	60	3	US-09-935-384-774	Sequence 774, App
870	6	0.8	46	4	US-10-424-599-192929	Sequence 192929,	943	60	3	US-10-166-698-5226	Sequence 5226, App
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872	6	0.8	46	4	US-10-424-599-284367	Sequence 284367,	945	60	4	US-10-424-599-217289	Sequence 217289,
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874	6	0.8	47	4	US-10-424-599-175289	Sequence 175289,	947	60	4	US-10-424-599-257530	Sequence 257530,
875	6	0.8	47	4	US-10-424-599-214676	Sequence 214676,	948	60	4	US-10-424-599-278739	Sequence 278739,
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877	6	0.8	49	4	US-10-425-115-201029	Sequence 201029,	950	60	4	US-10-240-801A-15	Sequence 15, App
878	6	0.8	49	4	US-10-425-115-212882	Sequence 212882,	951	60	4	US-10-437-963-145637	Sequence 145637,
879	6	0.8	49	4	US-10-425-115-343792	Sequence 343792,	952	60	4	US-10-490-917-1	Sequence 1, Appl
880	6	0.8	50	4	US-10-424-599-142892	Sequence 142892,	953	60	4	US-10-425-115-249337	Sequence 249337,
881	6	0.8	50	4	US-10-437-963-143258	Sequence 143258,	954	60	4	US-10-425-115-258455	Sequence 258455,
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886	6	0.8	50	4	US-10-425-115-345542	Sequence 345542,	959	61	4	US-10-425-115-225088	Sequence 225088,
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889	6	0.8	51	3	US-09-738-626-4205	Sequence 4205, App	962	62	4	US-10-424-599-178215	Sequence 178215,
890	6	0.8	51	4	US-10-424-599-198733	Sequence 198733,	963	62	4	US-10-424-599-244018	Sequence 244018,
891	6	0.8	51	4	US-10-424-599-192988	Sequence 192988,	964	62	4	US-10-424-599-246325	Sequence 246325,
892	6	0.8	51	4	US-10-425-115-229574	Sequence 229574,	965	62	4	US-10-425-115-226730	Sequence 226730,
893	6	0.8	51	4	US-10-425-115-281091	Sequence 281091,	966	62	4	US-10-425-115-251725	Sequence 251725,
894	6	0.8	52	3	US-09-764-847-804	Sequence 804, App	967	62	4	US-10-425-115-280551	Sequence 280551,
895	6	0.8	52	4	US-10-029-154-804	Sequence 154, App	968	63	3	US-09-864-761-48451	Sequence 48451, A
896	6	0.8	52	4	US-10-029-386-32686	Sequence 32686, A	969	63	3	US-09-738-626-5130	Sequence 5130, App
897	6	0.8	52	4	US-10-424-599-210870	Sequence 210870,	970	63	3	US-09-738-626-5130	Sequence 5130, App
898	6	0.8	52	4	US-10-424-599-241749	Sequence 241749,	971	63	4	US-10-074-095-354	Sequence 354, App
899	6	0.8	52	4	US-10-437-963-135363	Sequence 135363,	972	63	4	US-10-215-872-354	Sequence 354, App
900	6	0.8	52	4	US-10-437-963-183149	Sequence 183149,	973	63	4	US-10-424-599-198003	Sequence 198003,
901	6	0.8	52	4	US-10-767-701-59635	Sequence 59635, A	974	63	4	US-10-424-599-232260	Sequence 232260,
902	6	0.8	53	4	US-10-424-599-233874	Sequence 233874,	975	63	4	US-10-424-599-239634	Sequence 239634,
903	6	0.8	53	4	US-10-425-115-209875	Sequence 209875,	976	63	4	US-10-425-115-185582	Sequence 185582,

977	6	0.8	63	4	US-10-425-115-207449	Sequence 207449,
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979	6	0.8	63	4	US-10-425-115-293345	Sequence 293345,
980	6	0.8	64	4	US-10-349-607-130	Sequence 130, App
981	6	0.8	64	4	US-10-424-599-154815	Sequence 154815,
982	6	0.8	64	4	US-10-425-115-234850	Sequence 234850,
983	6	0.8	64	4	US-10-425-115-255147	Sequence 255147,
984	6	0.8	64	4	US-10-425-115-312105	Sequence 312105,
985	6	0.8	65	3	US-09-864-761-39981	Sequence 39981, A
986	6	0.8	65	4	US-10-001-870-119	Sequence 119, App
987	6	0.8	65	4	US-10-097-111-388	Sequence 388, App
988	6	0.8	65	4	US-10-425-115-279901	Sequence 279901,
989	6	0.8	65	5	US-10-856-499-604	Sequence 604, App
990	6	0.8	66	4	US-10-424-599-193996	Sequence 193996,
991	6	0.8	66	4	US-10-424-599-198991	Sequence 198991,
992	6	0.8	66	4	US-10-424-599-223134	Sequence 223134,
993	6	0.8	66	4	US-10-425-115-336417	Sequence 336417,
994	6	0.8	67	4	US-10-156-761-8250	Sequence 8250, Ap
995	6	0.8	67	4	US-10-424-599-160950	Sequence 160950,
996	6	0.8	67	4	US-10-424-599-261870	Sequence 261870,
997	6	0.8	67	4	US-10-424-599-266764	Sequence 266764,
998	6	0.8	67	4	US-10-425-115-313696	Sequence 313696,
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ALIGNMENTS						
RESULT 1						
US-09-994-192-4						
; Sequence 4, Application US/09994192						
; Publication No. US20020086028A1						
; GENERAL INFORMATION:						
; APPLICANT: Judd, Ralph C.						
; APPLICANT: Manning, Scott D.						
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis						
; FILE REFERENCE: UMSBC147AUSA						
; CURRENT APPLICATION NUMBER: US/09/994,192						
; PRIOR FILING DATE: 2001-11-26						
; PRIOR FILING DATE: 1998-10-22						
; NUMBER OF SEQ ID NOS: 8						
; SOFTWARE: Patent in version 3.1						
; SEQ ID NO 4						
; LENGTH: 797						
; TYPE: PRT						
; ORGANISM: Neisseria meningitidis						
US-09-994-192-4						
Query Match 100.0%; Score 797; DB 3; Length 797;						
Best Local Similarity 100.0%; Pred. No. 0;						
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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Qy	61	IIKSLYATGFFDDVRVETADGQLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ	120			
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Qy	121	SOYFNQATLNOAAGLKEEYLGRLKNIQITPKVTKLARNRVDITIDEGSAKITDIE	180			
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Qy	181	PEGNQVTSDRKLMQMSLTGEGITWLTNRNQFNEQFAQDMKVTDFYQNGYDFRIL	240			
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Qy	241	DTDIQTNEDKTKQTIKITVHEGGRFRWGVKSIEGDTNEVPKAELEKLLTWKPGKMYERQ	300			

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Db	781	KPEDEIQRFQFQLGTTFF 797	
RESULT 2			
US-10-606-618-4			
; Sequence 4, Application US/10606618			
; Publication No. US20050074458A1			
; GENERAL INFORMATION:			
; APPLICANT: Judd, Ralph C.			
; APPLICANT: Manning, Scott D.			
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis			
; FILE REFERENCE: UMSBC147AUSA			
; CURRENT APPLICATION NUMBER: US/10/606,618			
; CURRENT FILING DATE: 2003-06-26			
; PRIOR FILING DATE: US/09/994,192			
; PRIOR FILING DATE: 2001-11-26			
; PRIOR APPLICATION NUMBER: US 09/177,039			
; PRIOR FILING DATE: 1998-10-22			
; NUMBER OF SEQ ID NOS: 8			
; SOFTWARE: Patent in version 3.1			
; SEQ ID NO 4			
; LENGTH: 797			
; TYPE: PRT			
; ORGANISM: Neisseria meningitidis			
US-10-606-618-4			
Query Match 100.0%; Score 797; DB 5; Length 797;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy 601 L P G S K L O Y S A T G R V Q N I Y G A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K F R Y A Y P L K K 780
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Db 661 G Y E S G T L G P K V Y D E Y G E K I S Y G G N K K A N V S A E L L F P M P G A K D A R T V R L S L F A D A G S V M D G 720
Qy 721 K T Y D N S S A T G R V Q N I Y G A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K F R Y A Y P L K K 780
Db 721 K T Y D N S S A T G R V Q N I Y G A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K F R Y A Y P L K K 780
Qy 781 K P E D E I Q R F Q F O L G T T F 797
Db 781 K P E D E I Q R F Q F O L G T T F 797

RESULT 3
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-3

Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 A D T T I Q D I R V E G L Q R T E P S T V F N Y L P V K Y C D T Y N D T H G S A I I K S L Y A T G F D D V R V E T A D 80
Db 21 A D T T I Q D I R V E G L Q R T E P S T V F N Y L P V K Y C D T Y N D T H G S A I I K S L Y A T G F D D V R V E T A D 80
Qy 81 G O L L L T V I E R P T I G S L N I T G A K M L Q N D A I K N L E S F G L A Q S O Y F N Q A T L N Q A V A G L K E E Y 140
Db 81 G O L L L T V I E R P T I G S L N I T G A K M L Q N D A I K N L E S F G L A Q S O Y F N Q A T L N Q A V A G L K E E Y 140
Qy 141 L G R G K L N I Q I T P K V T K L A R N R V D I D I I D E G K S A K I T D I E F E G N Q V S D R K L M R Q M S L I T E 200
Db 141 L G R G K L N I Q I T P K V T K L A R N R V D I D I I D E G K S A K I T D I E F E G N Q V S D R K L M R Q M S L I T E 200
Qy 201 G G I T W T L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L D T D I Q T N E D K T Q I K I T V H 260
Db 201 G G I T W T L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L D T D I Q T N E D K T Q I K I T V H 260
Qy 261 E G G R F R M G K V S I E G D T N E V P K A E L K L T M K P G K W Y E R Q Q M T A V L G E I Q N R M G S A G Y A S 320
Db 261 E G G R F R M G K V S I E G D T N E V P K A E L K L T M K P G K W Y E R Q Q M T A V L G E I Q N R M G S A G Y A S 320
Qy 321 E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N N K T R D E V V R R E L R O M E S A P Y D T S 380
Db 321 E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N N K T R D E V V R R E L R O M E S A P Y D T S 380
Qy 381 K L O R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E R S T G S L D L S A G W Q D T G L V M 440
Db 381 K L O R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E R S T G S L D L S A G W Q D T G L V M 440
Qy 441 S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A D G V S L G Y D V Y G K A F D P R K A S 500
Db 441 S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A D G V S L G Y D V Y G K A F D P R K A S 500
Qy 501 T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T Y N K A P K H Y A D F I K K Y G K T D G 560
Db 501 T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T Y N K A P K H Y A D F I K K Y G K T D G 560
Qy 561 T D G S F K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A L P G S K L O Y S A T G R V Q N I Y G 620
Db 561 T D G S F K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A L P G S K L O Y S A T G R V Q N I Y G 620
Qy 621 L S K T F T L M L G E V G I A G Y G R T K E I P F F E N F Y G G L G S V R G Y E S G T L G P K V Y D E Y G E K I S 680
Db 621 L S K T F T L M L G E V G I A G Y G R T K E I P F F E N F Y G G L G S V R G Y E S G T L G P K V Y D E Y G E K I S 680
Qy 681 Y G G N K K A N V S A E L L F P M P G A K D A R T V R L S L F A D A G S V M D G K T Y D N S S A T G R V Q N I Y G 740
Db 681 Y G G N K K A N V S A E L L F P M P G A K D A R T V R L S L F A D A G S V M D G K T Y D N S S A T G R V Q N I Y G 740
Qy 741 A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K F 772
Db 741 A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K F 772

RESULT 4
US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02

```
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

Query Match      94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Qy 141 LGRGKLNITQITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLMQMSLTE 200
Db 141 LGRGKLNITQITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLMQMSLTE 200
Qy 201 GGIWTLTRSNQNEQKFAQDMKVDFYQNNGYDFRILDTDIOTNEDKTQTIKITVH 260
Db 201 GGIWTLTRSNQNEQKFAQDMKVDFYQNNGYDFRILDTDIOTNEDKTQTIKITVH 260
Qy 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Db 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIEPRKIIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPRKIIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQRSKERVLLGDFDNVQFPAVLPGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQRSKERVLLGDFDNVQFPAVLPGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500
Db 441 SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560
Qy 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWFFP 620
Db 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWFFP 620
Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIPIFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTKEIPIFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Qy 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
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RESULT 5
US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
```

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; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

Query Match      94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Db 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEY 140
Qy 141 LGRGKLNITQITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLMQMSLTE 200
Db 141 LGRGKLNITQITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLMQMSLTE 200
Qy 201 GGIWTLTRSNQNEQKFAQDMKVDFYQNNGYDFRILDTDIOTNEDKTQTIKITVH 260
Db 201 GGIWTLTRSNQNEQKFAQDMKVDFYQNNGYDFRILDTDIOTNEDKTQTIKITVH 260
Qy 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Db 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAVAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIEPRKIIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPRKIIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQRSKERVLLGDFDNVQFPAVLPGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQRSKERVLLGDFDNVQFPAVLPGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500
Db 441 SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKGTG 560
Qy 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWFFP 620
Db 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWFFP 620
Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIPIFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTKEIPIFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Qy 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGKNKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
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RESULT 6
US-10-181-600-3
; Sequence 3, Application US/10181600
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; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-181-600-3

Query Match      94.4%; Score 752; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 GOLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEY 140
Db 81 GOLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEY 140
Qy 141 LGRGKLNIOITPKVTYKLNARNVDITIDEGKSAKITDIEFEGNOVYSDRKLQMOMSLTE 200
Db 141 LGRGKLNIOITPKVTYKLNARNVDITIDEGKSAKITDIEFEGNOVYSDRKLQMOMSLTE 200
Qy 201 GGIWTWLTNRNQNEQFAQDMKVTDYFQNGGYDFRILDTIDQTNEDTKTQIKITVH 260
Db 201 GGIWTWLTNRNQNEQFAQDMKVTDYFQNGGYDFRILDTIDQTNEDTKTQIKITVH 260
Qy 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRMSGAGYAYS 320
Db 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRMSGAGYAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVVRRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVVRRRELQMESAPYDTS 380
Qy 381 KLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMNLSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMNLSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 500
Db 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKGTG 560
Qy 561 TDGSPKGMWLYKGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 620
Db 561 TDGSPKGMWLYKGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 620
Qy 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVYSGTGLPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVYSGTGLPKVYDEYGEKIS 680
Qy 681 YGNNKANVASBELLFPMPCAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVONIYG 740
Db 681 YGNNKANVASBELLFPMPCAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVONIYG 740
Qy 741 AGNTHKSTFTNELRYLSAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYLSAGGAVTWLSPGLPMKF 772
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Db 741 AGNTHKSTFTNELRYLSAGGAVTWLSPGLPMKF 772

RESULT 7
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-181-600-11

Query Match      94.4%; Score 752; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 GOLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEY 140
Db 81 GOLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEY 140
Qy 141 LGRGKLNIOITPKVTYKLNARNVDITIDEGKSAKITDIEFEGNOVYSDRKLQMOMSLTE 200
Db 141 LGRGKLNIOITPKVTYKLNARNVDITIDEGKSAKITDIEFEGNOVYSDRKLQMOMSLTE 200
Qy 201 GGIWTWLTNRNQNEQFAQDMKVTDYFQNGGYDFRILDTIDQTNEDTKTQIKITVH 260
Db 201 GGIWTWLTNRNQNEQFAQDMKVTDYFQNGGYDFRILDTIDQTNEDTKTQIKITVH 260
Qy 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRMSGAGYAYS 320
Db 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRMSGAGYAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVVRRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHITGNKTRDEVVRRRELQMESAPYDTS 380
Qy 381 KLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMNLSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMNLSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 500
Db 441 SAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKGTG 560
Qy 561 TDGSPKGMWLYKGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 620
Db 561 TDGSPKGMWLYKGTGSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKAS 620
Qy 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVYSGTGLPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSRVYSGTGLPKVYDEYGEKIS 680
Qy 741 AGNTHKSTFTNELRYLSAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYLSAGGAVTWLSPGLPMKF 772
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Qy 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
RESULT 8
US-10-988-943-7
; Sequence 7, Application US/10988943
; Publication No. US20050176085A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: METHOD OF SELECTIVE PEPTIDE ISOLATION FOR THE
; TITLE OF INVENTION: IDENTIFICATION AND QUANTITATIVE ANALYSIS OF PROTEINS IN
; TITLE OF INVENTION: COMPLEX MIXTURES.
; FILE REFERENCE: Proteomics CU2003-269
; CURRENT APPLICATION NUMBER: US/10/988,943
; CURRENT FILING DATE: 2004-11-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis (group B)
US-10-988-943-7
Query Match 94.4%; Score 752; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 ADFTIQDIRVEGLQRTPESTVFVNLVPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Db 21 ADFTIQDIRVEGLQRTPESTVFVNLVPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETAD 80
Qy 81 QQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140
Db 81 QQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140
Qy 141 LGRKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 200
Db 141 LGRKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 200
Qy 201 GGIWTWLTNRNQNEQFAQDMKVTDIFYQNGGYDFDRIILDTDIQTNEDTKQTIKITVH 260
Db 201 GGIWTWLTNRNQNEQFAQDMKVTDIFYQNGGYDFDRIILDTDIQTNEDTKQTIKITVH 260
Qy 261 EGGFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSGAGYAYS 320
Db 261 EGGFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSGAGYAYS 320
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKTDEVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKTDEVRRELQMESAPYDTS 380
Qy 381 KLQSKERVEVLLGYFDNVQFQDAVPLAGTDPKVDLNLMSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQSKERVEVLLGYFDNVQFQDAVPLAGTDPKVDLNLMSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYVKAFDPRKAS 500
Db 441 SAGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYVKAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFICKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFICKYKGTG 560
Qy 561 TDGSGFKGWLKGTGVGGRNKTDSALMPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSGFKGWLKGTGVGGRNKTDSALMPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620

Qy 621 LSKTFTMLGGVGIAGGYRTKEIPFPENFYGGGLGSVRGYESCTLGPVKYVDEYGEKLS 680
Db 621 LSKTFTMLGGVGIAGGYRTKEIPFPENFYGGGLGSVRGYESCTLGPVKYVDEYGEKLS 680
Qy 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGPMKF 772
RESULT 9
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5
Query Match 94.2%; Score 751; DB 4; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 DFTIQDIRVEGLQRTPESTVFVNLVPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFVNLVPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEYL 120
Qy 142 GRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 201
Db 121 GRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE 180
Qy 202 GIWTLWLTNRNQNEQFAQDMKVTDIFYQNGGYDFDRIILDTDIQTNEDTKQTIKITVHE 261
Db 181 GIWTLWLTNRNQNEQFAQDMKVTDIFYQNGGYDFDRIILDTDIQTNEDTKQTIKITVHE 240
Qy 262 GGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSGAGYAYS 321
Db 241 GGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQMTAVLGEIQNRMSGAGYAYS 300
Qy 322 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKTDEVRRELQMESAPYDTSK 381
Db 301 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKTDEVRRELQMESAPYDTSK 360
Qy 382 LQSKERVEVLLGYFDNVQFQDAVPLAGTDPKVDLNLMSLTERSTGSLDLSAGWQDTGLVMS 441
Db 361 LQSKERVEVLLGYFDNVQFQDAVPLAGTDPKVDLNLMSLTERSTGSLDLSAGWQDTGLVMS 420
Qy 442 AGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYVKAFDPRKAST 501
Db 421 AGVSQNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYVKAFDPRKAST 480
Qy 502 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFICKYKGTGDT 561

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Db 481 SIKQYKTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKYGKTDGT 540
Qy 562 DGSFKGWLKGTGWRNKTDLSALWPRGVLTVGNABIALPGSKLOYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGWRNKTDLSALWPRGVLTVGNABIALPGSKLOYYSATHNQTFWFFPL 600
Qy 622 SKTFTMLGGVGAGGRTKEIPFPENFYGGGLGVRGYESGTGLPKVYDEYGEKISY 681
Db 601 SKTFTMLGGVGAGGRTKEIPFPENFYGGGLGVRGYESGTGLPKVYDEYGEKISY 660
Qy 682 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
Db 661 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 721 GNTHKSTFTNELRYSGAGVATWLSPLGPMKF 751

RESULT 10
US-10-181-660-13
; Sequence 13, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 13
; TYPE: PRT
; LENGTH: 776
; ORGANISM: Neisseria meningitidis
US-10-181-660-13

Query Match 94.2%; Score 751; DB 4; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDRVVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDRVVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESGLAQSYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESGLAQSYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNQVYSDRKLQMSLTGEG 201
Db 121 GRGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNQVYSDRKLQMSLTGEG 180
Qy 202 GIWTLTRSNQNEQKFAQDMKVTDFYQNNGYDFPRILDTDIQNEDEKTKITITVHE 261
Db 181 GIWTLTRSNQNEQKFAQDMKVTDFYQNNGYDFPRILDTDIQNEDEKTKITITVHE 240
Qy 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 321
Db 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 300
Qy 322 ISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 381
Db 301 ISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 360
Qy 382 LQRSKERVLLGYFDNVQDVAFLAGTDPKVDLNMSLTERSTGSLDSAGWQDGLVMS 441
Db 361 LQRSKERVLLGYFDNVQDVAFLAGTDPKVDLNMSLTERSTGSLDSAGWQDGLVMS 420
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Qy 442 AGVSQDNLFOTGSAALRASRSKTTTLNGSLSFPTDPIFTADGVSLGYDVYKAFDPRKAST 501
Db 421 AGVSQDNLFOTGSAALRASRSKTTTLNGSLSFPTDPIFTADGVSLGYDVYKAFDPRKAST 480
Qy 502 SIKQYKTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKYGKTDGT 561
Db 481 SIKQYKTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKYGKTDGT 540
Qy 562 DGSFKGWLKGTGWRNKTDLSALWPRGVLTVGNABIALPGSKLOYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGWRNKTDLSALWPRGVLTVGNABIALPGSKLOYYSATHNQTFWFFPL 600
Qy 622 SKTFTMLGGVGAGGRTKEIPFPENFYGGGLGVRGYESGTGLPKVYDEYGEKISY 681
Db 601 SKTFTMLGGVGAGGRTKEIPFPENFYGGGLGVRGYESGTGLPKVYDEYGEKISY 660
Qy 682 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
Db 661 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 721 GNTHKSTFTNELRYSGAGVATWLSPLGPMKF 751

RESULT 11
US-10-181-600-5
; Sequence 5, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-5

Query Match 94.2%; Score 751; DB 5; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDRVVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDRVVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESGLAQSYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESGLAQSYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNQVYSDRKLQMSLTGEG 201
Db 121 GRGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNQVYSDRKLQMSLTGEG 180
Qy 202 GIWTLTRSNQNEQKFAQDMKVTDFYQNNGYDFPRILDTDIQNEDEKTKITITVHE 261
Db 181 GIWTLTRSNQNEQKFAQDMKVTDFYQNNGYDFPRILDTDIQNEDEKTKITITVHE 240
Qy 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 321
Db 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOMTAVLGIEIQNRMSAGYAYSE 300
Qy 322 ISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 381
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Db 301 ISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 360
Qy 382 LQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 441
Db 361 LQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 420
Qy 442 AGVSQDNLFGTGSAALRASRSKTTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 501
Db 421 AGVSQDNLFGTGSAALRASRSKTTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 480
Qy 502 SIKQYKTTTAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 561
Db 481 SIKQYKTTTAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 540
Qy 562 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 600
Qy 622 SKTFTLMLGGEVGTAGGYGRTKETIPEFFENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 681
Db 601 SKTFTLMLGGEVGTAGGYGRTKETIPEFFENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 660
Qy 682 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
Db 661 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 751

RESULT 12
US-10-181-600-13
; Sequence 13, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-13
```

```
Query Match 94.2%; Score 751; DB 5; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSQYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSQYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNQITPKVTKLARNRVDDIITIDEGSAKITDIEPEGNQVYSDRKLQMSLTEG 201
Db 121 GRGKLNQITPKVTKLARNRVDDIITIDEGSAKITDIEPEGNQVYSDRKLQMSLTEG 180
Qy 202 GIWTLNRSQNFQEKPAQDMKEKVTDFYQNNGYFDFRLLDITDITNEDKTKQTIKIIVHE 261
Db 181 GIWTLNRSQNFQEKPAQDMKEKVTDFYQNNGYFDFRLLDITDITNEDKTKQTIKIIVHE 240
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Qy 262 GGRFRMGKVISIEGDTNEVPKAELEKLLTMKPGKWYERQOQMTAVLGEIONRMSGAGYAYSE 321
Db 241 GGRFRMGKVISIEGDTNEVPKAELEKLLTMKPGKWYERQOQMTAVLGEIONRMSGAGYAYSE 300
Qy 322 ISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 381
Db 301 ISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSK 360
Qy 382 LQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 441
Db 361 LQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 420
Qy 442 AGVSQDNLFGTGSAALRASRSKTTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 501
Db 421 AGVSQDNLFGTGSAALRASRSKTTTLNGSLSFDPYFTADGVSIGYDVYKAFDPRKAST 480
Qy 502 SIKQYKTTTAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 561
Db 481 SIKQYKTTTAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFIKKYKTDGT 540
Qy 562 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 621
Db 541 DGSFKGWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQTFWFFPL 600
Qy 622 SKTFTLMLGGEVGTAGGYGRTKETIPEFFENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 681
Db 601 SKTFTLMLGGEVGTAGGYGRTKETIPEFFENFYGGGLGSRVGYESGTLGPKYVDEYGEKISY 660
Qy 682 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
Db 661 GGNKANVSAELLFPMPGAADARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 751

RESULT 13
US-10-181-660-7
; Sequence 7, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181.660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-7
```

```
Query Match 26.3%; Score 210; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQ 120
Qy 121 SOYFNQATLNQAVAGLKEEYVGRGKLNQITPKVTKLARNRVDDIITIDEGSAKITDIE 180
```



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Db      121  SOYFNOATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITDEGKSAKITDIE 180
Qy      181  PEGNOVYSDRKLMRQMSLTEGGIWTWLTTRS 210
Db      181  PEGNOVYSDRKLMRQMSLTEGGIWTWLTTRS 210
Db      181  PEGNOVYSDRKLMRQMSLTEGGIWTWLTTRS 210

RESULT 14
US-10-181-600-7
; Sequence 7, Application US/10181660
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-7
```

```
Query Match      26.3%; Score 210; DB 5; Length 792;
Best Local Similarity 100.0%; Pred. No. 2e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MKLQIASALMMLGTSPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db      1  MKLQIASALMMLGTSPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy      61  IIKSLYATGFFDDVRVETADGQLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db      61  IIKSLYATGFFDDVRVETADGQLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy      121  SOYFNOATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITDEGKSAKITDIE 180
Db      121  SOYFNOATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITDEGKSAKITDIE 180

Qy      181  PEGNOVYSDRKLMRQMSLTEGGIWTWLTTRS 210
Db      181  PEGNOVYSDRKLMRQMSLTEGGIWTWLTTRS 210
```

```
RESULT 15
US-10-181-660-9
; Sequence 9, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181.660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-9
```

```
Query Match      23.7%; Score 189; DB 4; Length 771;
```

```
Best Local Similarity 100.0%; Pred. No. 1.6e-178;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22  DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db      1  DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60

Qy      82  QLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 141
Db      61  QLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 120

Qy      142  GRGKLNIIQITPKVTKLARNRVDIDITDEGKSAKITDIEPEGNOVYSDRKLMRQMSLTEG 201
Db      121  GRGKLNIIQITPKVTKLARNRVDIDITDEGKSAKITDIEPEGNOVYSDRKLMRQMSLTEG 180

Qy      202  GIWTLTTRS 210
Db      181  GIWTLTTRS 189
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